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Release 2. Copyright Di	1D John F. Collins, Biocomputing Researc (c) 1993, 1994, 1995 University of Edin stribution rights by IntelliGenetics, In
MPsrch_nn n.a.	- n.a. database search, using Smith-Waterman algorithm
ar output in	ייטר אַפּוועזמרפּט.
Title: Description: Perfect Score: N.A. Sequence: Comp:	>US-08-320-157-6 (1-2094) from US08320157.seq 2094 1 GAGGATCTACAGGGGACAAGCAAAAAAAAAA
Scoring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0; Query 0
Searched:	362067 seqs, 549138275 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	embl-new3 1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
Database:	3:BCT2 20:BCT3 21:BCT4 22 5:BCT9 27:BCT10 28:BCT11 5:HTG1 33:HTG2 34:HTG3 14:HTG3 14:H
	3:INV5 40:INV6 41:INV7 42:INV8 43:INV9 46:INV8 43:INV9 46:INV8 43:INV9 46:INV8 43:INV9 46:INV8 43:INV9 46:INV8
	72:PRI3 73:PRI4 74:PRI5 75:PRI6 76:PRI7 77:PRI8 78:PRI9 79:PRI10 80:PRI11 81:PRI12 82:PRI13 83:PRI14 84:PRI15 85:ROD1 86:ROD2 87:ROD3 88:ROD4 89:ROD5 90:ROD5 91:ROD7 92:ROD8 93:STR 94:SYN 95:UNA 96:VRL1 97:VRL2 98:VRL3 99:VRL4 100:VRL5 101:VRL5 102:VRL7 103:VRL8 104:VRL9
Database:	3 27:GEN1 108:GEN2 13:VRT 114:PHG 1
Database:	120:UNA
Statistics:	Mean 11.818; Variance 4.529; scale 2.609

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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nology Inc., 1401 Marina Way Sc
Location/Qualifiers
1.20gailsm-"Homo sapiens"
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201..836
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Similarity 100.0%;
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Richmond, CA 94804, USA
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (basea 1 to 6478)
Kiefer, M.C., Brauer, M.J., Powers, V.C., Wu, J.J., Umansky, S.R.,
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vortebrata; Eutheria; Primates; Catarrhini; Hominidae; Hom
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Lutz, R.J., Evan, G.I. and Guild, B.C.
Induction of apoptosis by the Bcl-2 homologue Bak
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Chittenden,T.
Direct Submission
Submitted (30-MAR-1995) Thomas Chittenden, Apopto
Inc., 148 Sidney St., Cambridge, MA 02139, USA
Location/Qualifiers
Ce /organism="Homo sapiens"
//colo=_lib="Jurkat cell cDNA library (St /celne_lib="Jurkat cell"
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/function="induction of apoptosis"
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ael C. Kiefer, Mol. Biol., LXR ina Way South, Richmond, CA 94804, USA he widely distributed Bcl-2 homologue 23; ageccataggccacccctatcctctgagt 1920 cctccagcccttgggaccttcaactccac 1595 496; DB 77; Length 5408; o. 0.00e+00; smatches 186; Indels 33; Gaps 19-AUG-1995 wers, V.C., Wu, J.J., Umansky, S.R., karyotes; Metazoa; Chordata; es; Catarrhini; Hominidae; Homo. Human genomic DNA" PRI lete cds. 1341 t 1995) iens" 1949 2076

2847 1381 2905 1441 2965	Db 3025 ctcagctctcccttcctctctctctatagatacttgctcccaacccattcactacagg 3084	Db 3145 CCCAGACTACAGGGCTLGGTTTAGGGTTTAGGGGGTAGAGGGGTAGGGGG 3204	Db 3264 tgggatcctccctcatggcacagtgtaatccagggtggagataggg-aactgt 3322 1	Db 3383 gtgtggggtgagagtaccttctctatcgggcacagcctagggtgtggggtgaagggg 3442 1 1 1 1 1 1 1 1 1	0-0 n z	ACCESSION X84213 NID 9804984 NID 9804984 KEYWORDS BC1-2 protein; CEBP-1 gene. SOURCE human. ORGANISM Homo sapiens Enkaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata, Butheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS Farrow, S.N., White, J.H., Martinou, I., Raven, T., Pun, K.T., Grinham, C.J., Martinou, J.C. and Brown, R. TITLE Cloning of a bc1-2 homologue by interaction with adenovirus E1B 19K JOURNAL Nature 374 (6524), 731-733 (1995) MEDLINE 95231652 REMARK Erratum:[Nature 1995 Jun 1;375(6530):431]] REMARK Erratum:[Nature 1995 Jun 1;375(6530):431]] AUTHORS Brown, R	TITLE Direct Submission JOURNAL Submitted (25-JAN-1995) R. Brown, Glaxo Research & Development, Greenford Road, Greenford, Middlesex UB6 OHE, UK FEATURES 11360
Db 1775 tacgttttttaccaccatcagcaggaacaggaggctgaagggcgccctgccgac 1834	1954 geageacctgeageceaeggeagagaacgectacgagtacttcaccaagategectccag 2013	2074 totggtcctacatgtctaccagcacggcttgactggcttcctgggcctggtgaccgctt	2191 ggtggcagccttggactttgggcaatatcccatcctgaacgtgctggtggttgtgggtgt	2311 ctttggggtcccagctgtgaccctgcctggacttaagccaagtctttgccttcccact	Db 2431 ggagggcccctgcgtggggccagtcaggctgcggaggcacctcaacattgcacggtgct 2490	Db 2551 cttagtcttgtctgctaggcgctgcagaggctgataacttggggaagcagggaa 2610	8-6 3-8 8-6 3-8	8 – K

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Order of segments is not known; 800 n's separate segments.

Onfinished sequence: dJ291.10 Contig_ID: 01371 Length: 3951 bp Unfinished sequence: dJ291.110 Contig_ID: 01622 Length: 1040 bp Unfinished sequence: dJ291.10 Contig_ID: 01422 Length: 1722 bp Unfinished sequence: dJ291.10 Contig_ID: 010105 Length: 26804 bp Unfinished sequence: dJ291.10 Contig_ID: 01527 Length: 1598 bp Unfinished sequence: dJ291.10 Contig_ID: 01231 Length: 1547 bp
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IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progr
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19-MAR-1997 (Rel. 51, Last updated, Version 1)
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193..828
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Direct Submission
Submitted (14-0CT-1996) to the DDBJ/EMBL/GenBank databases.
Hidetaka Eguchi, Saitama Cancer Center Research Institute,
Depertment of Blochemistry; 818 Komuro, Ina, Kita-adachi-gun,
Saitama 362, Japan (E-mail:hide4esaitama-cc.go.jp,
Tel:048-722-1111(ex.255), Fax:048-722-1739)
2 (bases 1 to 444)
Eguchi, H. and Rayashi, S.
Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL
and Bak, as well as susceptibility to therapeutic agents of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115382
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         1977 AGTICTIGATICAGCCAAATGCAGGGGGGGGGGGGGCAGATG-GAGCCCATAGGCCACCCC
                                                                            ctcagttctctcccttcctctcttatagacacttgctcccaacccattcactacagg
                                                                                                                     1561 CTCAGTTCTCTCCCTTCCTCTCTTATAGACACTTGCTCCCAACCCATTCACTAGAG
                                                                                                                                                                                                                                                                                                                                              catctggagggttctaagtgggagaaggactatcaacaccactaggaatcccagaggtgg
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Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 444)
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/clone="pGEMBak01-02"
join(D88396:26.90,51.231,358.>444)
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Human DNA for apotosis-regulator
D88397
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/db_xref="PID:g1655494"
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Unpublished (1996)
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                                                                                                                                                                                                                                               /organism="Homo sapiens"
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BP; 28765 A; 27932 C; 27951 G; 27528 T; 11403 other;
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    2194 bp
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      01408
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Pred. No. 0.00e+00;
0; Mismatches 1;
  Contig_ID:
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Unfinished sequence: dJ291J10 CC Unfinished sequence: dJ291J10 CC
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Best Local Similarity 98.8%;
Matches 1345; Conservative
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/db_xref="PID:e258462"
/db_xref="PID:g1673441"
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RVITGNIKASPSMYMEMFTDQNPQADQDLEETESDGAMNPTD"
/gene="Tsx"
                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 94459)
Simmler,M.C., Cunningham,D.B., Clerc,P., Vermat,T., Caudron,D.,
Cruaud,C., Pawlak,A., Szpirer,C., Weissenbach,J., Claverie,J.M. and
                                                                                                                                                                                                                                                                                                                                                                                                               A 94kb genomic sequence 3' to the murine Xist gene reveals an AT rich region containing a new testis specific gene Tsx Hun. Mol. Genet. In press
2 (bases 1 to 94459)
Claverie, J.
Direct Submission
Direct Submission
Submitted (06-AUG-1996) J. Claverie, Information Genetique & Structurale, CNRS EP 91, 31 Chemin Joseph Aiguier, 13402 Marseille Cedex 20, FRANCE
This gene constitutes one of the only well verified examples of a case where the AG-GT rule in not obeyed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(44627..44791,46180..46215,46896..46932,48355..48436,
50663..50763,52149..52207,54425..54741)
/gene-"Tsx"
44627..44791
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50663..50763,52149..52207,54425..54450)
/gene="Tsx"
                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                        15-NOV-1996
            Gaps
            ö
                                                                                                                                                                                                               encoding Tsx gene.
            Indels
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            Mismatches
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/organism="Mus_musculus"
                                                                                                                                                                                    MMTSXDNA 94459 bp DNA
M.musculus 94kb genomic sequence
X99946
                                                                                                 /clone_lib="YAC pa-2"
/map="D-E mu"
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/gene="Tsx"
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/translation="MLQHLQPTAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLA
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VLLGQFVVR"
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Submitted (14-0CT-1996) to the DDBJ/EMBL/GenBank databases.
Hidetaka Eguchi, Saitama Cancer Center Research Institute,
Hidetaka Eguchi, Saitama Romuro, Ina, Kita-adachi-gun,
Saitama 362, Japan (E-mail:hideGsaitama-cc.go.jp,
Tel:048-722-111(ex.255), Fax:048-722-1739)
Eguchi, H. and Hayashi, S.
                                                                                                                                                                                                                                                             Gaps
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eguchi, H.
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                                                                                                                                                                                                                              Length 444;
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Human DNA for apotosis regulator Bak, exon 1.
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Pred. No. 7.63e-161;
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Homo sapiens
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/clone="pGEMBak01-02"
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Best Local Similarity 100.0%;
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Best Local Similarity 99.0%;
Matches 191; Conservative
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996,
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Pred. No. 2.15e-10;
67; Mismatches 64; Indels
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Pred. No. 1.33e-19;
0; Mismatches 52; Indels
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50764..52148
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50663..50763
/gene="Tsx"
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52149..52207
/gene="Tsx"
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/gene="Tsx"
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/gene="Tsx"
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Best Local Similarity 67.7%;
Matches 113; Conservative
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Best Local Similarity 16.9%;
Matches 27; Conservative
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 215)

Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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PATENT: WO 9214485-A 11 03-SEP-1992;
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Pred. No. 1.58e-06;
74; Mismatches 89; Indels
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Mouse brain GAD sequence (MBGAD).
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/db_xref="PID:e204340"
/db_xref="PID:91247777"
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Matches 26; Conservative
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            KICGFLORTUSLEEKSRLVSAFRERÖSSKNLLSCENSDOGARRRTETDFSNLFADDL
LPAKNGEEQTAQFLLEVVDILLNYVRKTFDRSTKVLDFHHPHQLLEGMEGFNLELSDH
PESLEQILVDCRDTLKKGVRTGHPRFFNQLSTGLDIGLAGEWLTSTANTNMETYEIA
PVYLJMEQILYDCRDTLKKWRKIVGWSNKDGDGIFSPGGAISNMYSIMAARYKYFPEVTRKGMA
AVPKLVLFTSEHSHSYSTKAGAALGFCTDNYLLIKCNERGKIIPADEAKILDAKOKG
YVPLYVNATAGTTVYGAFDPIQEIADICEKYNLWLHVDAAWGGGLLMSRKHRHKLSGI
ERANSYTWNPHKMMGVLLQCSAILVKEKGILQGCNQMCAGYLFQPDKQYDVSYDTGDK
                                                                                                                                 AIQCGRHVDIFKFWLMMKAKGTVGFENQINKCLELADYLYAKIKNREEFEMVFDGEPE
HTNVCFWYIPQSLRGVPDSPERREKLHRVAPKIKALMMESGTTMVGYQPQGDKANFFR
MVISNPAATQSDIDFLIEEIERLGQDL"
translation="MASSTPSPATSSNAGADPNTINLRPTTYDTWCGVAHGCTRKLGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (21-OCT-1996) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                    1715 cagccgccacccagtctgacatcgatttcctcattgaggagatagagaggttgggccagg 1774
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Human 18q- syndrome breakpoint satellite III DNA recombination
sequence.
U19554
91098521
                                                                                                                                                                                                                                                                                                                      21-OCT-1996
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                                                                                                                                                                                                                                   Score 27; DB 54; Length 1782; Pred. No. 2.81e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 73; Length 459
Pred. No. 2.81e-02;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                     0; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSACO00028 45976 bp DNA 00023; HTGS phase 3, complete sequence. AC000028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
3 (bases 1 to 45976)
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Best Local Similarity 80.0%;
Matches 36; Conservative
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Best Local Similarity 71.4%;
Matches 45; Conservative
                                                                                                                                                                                    440 c
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Homo sapiens
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REFERENCE
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JOURNAL
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 257) Schneider, S.S., Trask, B.J., Overhauser, J. and Silverman, G.A. An 18q- syndrome breakpoint is located in a cluster of serpin genes and was formed by an illegitimate recombination with satellite III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2734)
Xie, Y.G., Han, F.Y., Peyrard, M., Ruttledge, M.H., Fransson, I.,
DeJong, P., Collins, J., Dunham, I., Nordenskjold, M. and Dumanski, J.P.
Cloning of a novel, anonymous gene from a megabase-range YAC and
cosmid contig in the neurofibromatosis type 2/meningioma region on
human chromosome 22q12
Hum. Mol. Genet. 2 (9), 1361-1368 (1993)
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/translation="MSSESSKKRKPKVIRSDGAPAEGKRNRSDTEQEGKYYSEEAEVD
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RLAHIRLKKGRDQTHEAKQKVDAYHLOLQNLLYEVMHLQKEIIKCLEFKSKHEEIDLV
SLEEFYKEAPPDISKAEVTMGDPHQQTLARLDWELEORKRLAEKYRECLSNKEKILKE
                                                                                                                                                                                                                                                                               Direct Submission
Submitted (06-JAN-1995) Gary A. Silverman, Pediatrics, Harvard
Medical School, Joint Program in Neonatology, 300 Longwood Avenue
Enders-9, Boston, MA 02115, USA
Location/Qualifiers
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/isolate="JL184. an 18q syndrome patient"
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Pred. No. 5.52e-01;
0; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="normal chromosome 18 DNA;
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/tissue_lib="Stratagene #936206"
/map="22q12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unknown filler sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="satellite III"
27 c 90 g 63 t
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1..2754
/organism="Homo sapiens"
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80..256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="18q21.3"
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L18972
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Best Local Similarity 71.2%;
Matches 42; Conservative
                                                                                                                                                                                                                                2 (bases 1 to 257)
Silverman, G.A.
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Homo sapiens
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IEVKKEYLSSLOPRLNSIMQASLPVQEYLFMPFDQAHKQYETARHLPPPLYVLFVQAT
AYGQACDKTLSYAIEGSYDEAKALFKPPEDSQDDESDSDAEEEGTTKRRPTLGVQLD
BYRKEMIKHPLSYMLDDIKCKDDSYLHUTFYTUMININTHYKRKVTTAMELITPISAG
DLLSPDSVLSCLYFQDBGKKTPNPANOYGLILLSDSTVLELGHPYLWYQKLGGL
HPPKEQPQQTVIADHSLSASHMETTMKLLKTRYQSRLALHKOPASLEGGIVPYTSDCQ
YLFPAKVYSRLYKWYTAHEDYMELHFTKDIYDAGLAGDTNLYYMALIERGTAKLQAA
VVLNPGYSSIPPIFQLCLNWKGEKTNSNDDNIRAMEGEVNYCKELCGPWPSHGLTN
QLQRLCVLLDVYLETESHDDSVEGPKEFPQEKWCLRLFRGPSRMKPFKYNHPQGFFSH
R,
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593 t 723 g 694 c æ 744 BASE COUNT ORIGIN

Score 25; DB 79; Length 2754; Pred. No. 5.52e-01; 0; Mismatches 22; Indels (Query Match
Bost Local Similarity 68.1%;
Matches 47; Conservative

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289 agaacggag 297 ||| |||| 1578 GGAAGGGAG 1570 엄 g

Search completed: Thu Aug 21 10:27:37 1997 Job time: 4382 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Thu Aug 21 10:27:57 1997; MasPar time 218.06 Seconds 944.863 Million cell updates/sec Run on:

Pabular output not generated.

>US-08-320-157-6 (1-2094) from US08320157.seq 2094 Description: Perfect Score:

1 GAGGATCTACAGGGGACAAG........CAAAAAAAAAAGGGAGATCC 2094 CTCCTAGATGTCCCCTGTTC......GTTTTTTTTTTTGCCTCTAGG Sequence: N.A.

TABLE default Scoring table:

Gap

134151 seqs, 49196315 bases x 2 Searched:

Dbase 0; Query 0

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STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

iparti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part22 23:part25 26:part26 27:part27 n-geneseq27

Mean 9.693; Variance 5.444; scale 1.780 Statistics: No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. No. score g

SUMMARIES

Result No.	Score	Query Match	å Query Match Length DB	DB	£1	Description	Pred. No.
	2094	100.0	2094	24	T42138	Bak gene.	0.00e+00
71	2072	98.9	2072	14	095492	Human Cdn-1 cDNA.	0.00e+00
m	1899	90.7	6511	14	095493	Human Cdn-2 DNA.	0.00e+00
4	1886	90.1	1968	19	T17375	Bcl-Y cDNA.	0.00e+00
L)	1496	71.4	5408	14	095494	Human Cdn-3 DNA.	0.00e+00
Ψ	883	42.2	1286	24	T42139	Bak-2 dene.	0.00e+00
0	95	4.5	1047	~	010572		4.06e-46
æ	1 78	3.7	1047	7	010572	Human Natriuretic Pep	2.35e-34
on	43	2.1	91	σ	051746	Oligonucleotide probe	1.89e-11
10	44	2.1	204	Н	N81164	Base substituted E.co	4.60e-12
c 11	45	2.1	204	-1	N81164	Base substituted E.co	1.11e-12
c 12	42	2.0	91	σ	051746	Oligonucleotide probe	7.69e-11
c 13	37	1.8	114	12	070465	Generic DNA sequence	7.46e-08
c 14	36	1.7	114	12	070468	Generic DNA sequence	2.86e-07
15	34	1.6	114	12	070466	Generic DNA sequence	4.05e-06
16	34	1.6	114	12	070465	Generic DNA sequence	4.05e-06

4.05e-06 4.05e-06	4.05e-06	4.05e-06	1.49e - 05	4.05e-06	1.95e-04	7	2.38e-03	ω.	2.38e-03	•	2.71e-02	2.71e-02	æ	8.86e-02	2.83e-01	2.83e-01	2.83e-01	2.83e-01	æ	8.86e-02	2.83e-01	2.69e+00	8.85e-01	8.85e-01	5e-	8.85e-01	
Generic DNA sequence Generic DNA sequence	C DNA		Generic DNA sequence	æ	Generic DNA sequence	Brain GAD #2.	Ballast Constituent c	10 1	DC43 TSAR library gen	TSAR library		TSAR library	Generic DNA sequence	HCV envelope region n	HCV envelope region n	TSAR-9 library genera	DC43 TSAR library gen	DC43 TSAR library qen		Retinoblastoma protei							
Q70469 Q70467 Q70468	070467	070466	070469	N71302	070470	070470	070472	070471	070472	070473	070473	028435	011195	051787	T13613	T13612	T13611	T13610	970471	035072	035072	T13585	T13612	T13610	113	067603	
212	12	12	12	7	12	12	12	12	12	12	12	Ŋ	7	^	21	21	21	21	12	ø	φ	71	21	21	σ	10	
114	114	114	114	3871	114	114	114	114	114	114	114	1782	36	33	74	75	81	82	114	265	565	99	75	82	2456	2492	
999	1.6	٠	•	٠	1.5	٠	٠	7.4	•	1.3	1.3	1.3	1.2	1.2	1.2	1.2	1.2	1.2	•	•	•	•	•	•	1.1	1.1	
3 3 3 4 4	34	34	33	34	31	32	53	30	53	28	27	27	26	26	25	22	25	22	56	56	25	23	24	24	24	24	
118	50	21	22	23	24	22	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	
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ALIGNMENTS

Human; Bak; apoptosis; latency; virus replication;
Epstein-Barr virus; BHRFl; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; dlagnostic; ss. ВР T 1 T42138 standard; cDNA; 2094 T42138; 22-FEB-1997 (first entry) Homo sapiens. Bak gene

Location/Qualifiers 1..200 /*tag= b /product= Bak protein 3'UTR 837..2094 201..836 *tag= Key 5'UTR CDS

/*tag= c WO9633416-A1.

24-OCT-1996. 19-APR-1996; U05639. 20-APR-1995; US-426529. (LXRB-) LXR BIOTECHNOLOGY INC. BART PJ, Kiefer MC; WPI; 96-485886/48. P-PSDB; W03668.

Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral protein

an

Disclosure: Fig 1; 24pp; English.

The sequence encodes Bak protein, which is a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The Bak gene is located on human chromosome-6 at 6p21-23. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral replication or

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961	1021 ggtgctagtgccctctctgggcccagggctgtggcgtctcctccctc			1201	1261 gtctatgttccccaggattcagctattctggaagatcagcaccctaagaatgggactag 1320 	1321 gacctgagcctggtcctggccgtccctaagcatgtgtcccaggagcaggacctactagga 1380	1381 gagggggccaaggtcctgctcaactctaccctgctcccattcctccctc	1441 tgcctttgcagttggactctcagggattctgggcttggggtgtggggtggggtggagtcg 1500 1441 tgcctrrccagttggactctcagggattcrccgcrrcccgcrrcccgcrcccgrcrccaggrcrccgcrcrccaggcrrccgcgrcrccgcgrcrccaggrcrccgcgrcrccgcgrcrccaggrcrccgcgrcrccaggrcrccaggrcrccaggrcrccgcgrcrccaggrcrcaggrcrca	1501 cagaccagagctgtctgaactcacgtgtcagaagcctccaagcctgcct	1561 ctoagtictccccticctctcttatagacacttgctcccaacccaticactacagg 1620	1621 tgaaggeteteaeceatecetgggggeettgggtgattggetgetaaggeteetettg 1680 	1681 cccagactacagggcttaggacttggtttgttatatcagggaaaaggagtagggagttca 1740 	1741 tctggagggttctaagtgggagagtatcaacaccactaggaatcccggaggtggat 1800 	1801 cctcctcatggctctggcacagtgtaatccaggggtgtagtgggggaactgtgaatac 1860	1861 ttgaactctgttccccacctccatgctcctcaccgtctaggtctcctcagggtggg 1920 1861 trgaactcrgftccccaccctccargctcrcaccggtggg 1920 1861 trgaactcrgtrccccaccctccargctccrcaccrcacc	1921 ggtgacagtgccttctctattggcacagcctagggtcttgggggtcaggggggagagtt 1980 	1981 cttgattcagccaatgcagggagggaggcagatggagccataggccaccctatcc 2040
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CC latency in the absence of apoptosis. Compounds which inhibit the CC interaction may be used as virucide, antitumour or diagnostic agents. SQ Sequence 2094 BP; 410 A; 608 C; 606 G; 470 T;	Query Match 100.0%; Score 2094; DB 24; Length 2094; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 2094; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	3ccca 60	Db 61 ttcctggaaactgggctccactcagcccctgggagcagccagc	Db 121 tccatctccacctgctgagccacccgggttgggccaggatcccggcaggctgatcccgt 180	Db 181 cctccactgagacctgaaaatggcttcggggcaaggcccaggtcctcccaggcagg	Db 241 goggagagcctgccctctgcttctgaggagcaggtagcccaggacacagagagg 300	tggetg 	agcaccatgg 	421 tgggacggcagctcgccatcatcggggacgacatcaaccgacgctatgactcagagttcc 	481 agaccatgttgcagcacctgcagcccacggcagagaatgcctatgagtacttcaccaaga 	agoctgtttgagagtggcatcaattggggccgtgtggtggtgctttttgggct 	tacacgtctaccagcatggcctgactggcttcctaggccagg 	661 tgaccogcttcgtggtcgacttcatgctgcatcactgcattgcccggtggattgcacaga	721 ggggtggctggcagccctgaacttgggcaatggtcccatcctgaacgtgctggtgg	Db 781 ttctgggtgtggttctgttgggcagtttgtggtacgaagattcttcaaatcatgactcc 840 	841 caagggtgcctttgggtcccggttcagaccctgcctggacttaagcgaagtcttgcc 	tcccttgcagggtccccctcaagagtacagaagctttagcaagtgtgcact

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Claim 4; Fig.3A-C; 66pp; English.
Claim 4; Fig.3A-C; 66pp; English.
Cdn-1 cDNA was isolated from a human heart cDNA library using a previously isolated clone as probe. Recombinant Cdn-1 was produced in 5f9 and human colon adenocarcinoma HT29 cells. Expression of Cdn-1 in MI-LZ lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
Sequence 2072 BP; 404 A; 603 C; 598 G; 467 T;
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                                                                        hepatitis, osteoporosis;
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                                                                immunotherapy; therapy;
Indels
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Pred. No. 0.00e+00;
0; Mismatches 0;
                                                                         injury;
                                                               Cdn-1; apoptosis modulator; adoptive
autoimmune disease; reperfusion injur
shock; lymphoma; eczema; ss.
                                                                                               Location/Qualifiers
188..903
                                                                                                                                            30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
BARY PJ. Kiefer MC;
WPI; 95-215106/28.
                                2072
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Best Local Similarity 100.0%;
Matches 2072; Conservative
                                                (first entry)
                                standard; cDNA;
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W09515084-A.
08-JUN-1995.
30-NOV-1994; U13930.
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                                                        gcttaggacttggtttgttatatcagggaaaaggagtagggagttcatctggagggttct
                                                                                               Human Cdn-2 DNA.
Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema; ss.
Homo sapiens.
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Claim 6; Fig.5A-H; 66pp; English.
Claim 6. Fig.5A-H; 66pp; English.
Cdn-2 cDNA was isolated from a human placental genomic library using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (R77876).
Sequence 6511 BP; 1513 A; 1620 C; 1605 G; 1773 T;
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30-NOV-1994; U13930.
30-NOV-1994; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
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095493 standard; DNA; 6511 (095493;
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Best Local Similarity 97.3%;
Matches 2026; Conservative
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WPI; 95-215106/28.
P-PSDB; R77877.
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p prods. for cell proliferation
                                                                                                                                              Claim 5; Fig 4; 100pp; English.

A full-length cDNA clone (T17375) codes for Bcl-Y (R81451), a profein that induces apoptosis in cells and functions as a negative regulator of Bcl-2 function. It was isolated from a Jurkat cell CDNA library using as probe a partial Bcl-Y cDNA clone obtd. by PCR of DNA derived from the Namalwa cell line. The cDNA can be use for prodn. of recombinant Bcl-Y, as a probe, to produce transgenic animal models, and in the gene therapy of disorders characterised b inappropriate cell proliferation or cell death.

Sequence 1968 BP; 382 A; 560 C; 576 G; 450 T;
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larity 99.5%;
Conservative
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09-AUG-1994; US-287427
11-OCT-1994; US-321071
(IMMU-) IMMUNOGEN INC.
                                                                                                                                                                                                                                                       Similarity
                                                                                            Chittenden TD;
WPI; 96-139648/14.
P-PSDB; R81451.
 SS.
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WO9605232-A1.
22-FEB-1996.
                                                                                                                                         death
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nes 1940;
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02-JUL-1996 (first entry)
Bcl-Y cDNA.
Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis;
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W05915084-A

08-JUN-1995.

30-NOV-1994; U13930.

30-NOV-1994; US-320157.

(LXRB-) LX BIOPECHNOLOGY INC.

BAIT PJ, Kiefer WC;

WPI: 95-215106/28.
                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                  Human Cdn-3 DNA.
Cdn-3; apoptosis modulator;
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Best Local Similarity 89.6%;
Matches 1880; Conservative
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Q95494 standard; DNA; 5408
Q95494;
21-NOV-1995 (first entry)
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Sequence 5408 BP; 1369 A; 1384 C; 1314 G; 1341 T; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema; ss. Score 1496; DB 14; Length 5408; Pred. No. 0.00e+00; 0; Mismatches 186; Indels 33;

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19-APR-1996;
20-APR-1995;
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Epstein-Barr Virus; BHRF1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic;
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Domain 479..1047
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id -site 244..246
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23-JUN-1989; US-370673.
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Modified -site 195..1
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Modified -site 35..37
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Modified -site 161..1
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                                                                                    The sequence encodes Bak. Superior, which is a bc1-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The Bak-2 gene is located on human chromosome-20. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction and absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or disquostic agents. Sequence 1286 BP; 298 A; 341 C; 328 G; 319 T;
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                                          Screening for anti-viral agents - by detecting the ability of
                                                       agent to disrupt the interaction of a Bak protein and a viral
                                                                                                                                                                                                                                                Match 42.2%; Score 883; DB 24; Length 1286; Local Similarity 98.1%; Pred. No. 0.00e+00; os 916; Conservative 0; Mismatches 15; Indels 3
                                                                             Disclosure; Fig 2; 24pp; English.
(LXRB-) LXR BIOTECHNOLOGY INC
           Barr PJ, Kiefer MC;
WPI; 96-485886/48.
                               P-PSDB; W03669
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                                     852 TITGGGTCCCGGTTCAGACCCCTGCCTGGACTTAAGCGAAGTCTTTGCCTTCTCTGTTCC 911
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The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanyl cyclase. Homo sapiens.
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                                                                                                                                                                                                                                                                                         1047 TGGGCCCAGAGAGAGGGCACTAGCACCATGCAATGTTGAGGTGCCTCTGCAGCCTGACTG
     can
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 Antibodies with affinity for NPRB
                                                     Length 1047;
                                                                            Conservative 293; Mismatches 618; Indels
                              51 T;
                                                 Score 95; DB 2; I
Pred. No. 4.06e-46;
                           83 G;
                           15 C;
                          87 A;
                                                    4.58;
affinity chromatography. also be prepd.
                          1047 BP;
                                                                Local Similarity
les 93; Conser
               prepd
                            Seguence
                                                     Query Match
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Matches
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Gaps 10;
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The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having gnayl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                       UI Standard; DNA; 1047 BP.
010572;
010572;
09-APR-1991 (first entry)
Human Natriuretic Poptide Receptor B.
Hyperaldosteronism; glaucoma; guanyl cyclase.
                         218
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274 TCCTCAGAAGCAGGGCAGGCTCTCCGCACTCCTGGGAGGACCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 8.8%; Pred. No. 2.35e-34;
Matches 72; Conservative 234; Mismatches 503; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natriuretic protein receptor B - for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.7%; Score 78; DB 2; Length 1047; 8.8%; Pred. No. 2.35e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "binds natriuretic peptides A,B and C]"
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ified -site 24..26
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extracellular domain
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Chang M, Goeddel D, Lowe D;
WPI; 91-036711/05.
N-PSDB; Q10324.
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/label= N-glycos_site
Modified -site 195..197
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ied -site 244..246
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Modified -site 277..279
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4odified -site 349..351
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4odified -site 600..602
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23-JUN-1989; US-370673.
                                                                                                                                                                                                                                                                                                                                   /label= signal sequence
Protein 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified -site 24..26
/label= N-glycos_site
Modified -site 35..37
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269 TGAGGAGCAGGTAGCCCAGGACACAGAGGTTTTTCCGCAGCTACGTTTTTTACCGCCA 328
                                                                                                                                                  yhgytgnyvmdknndrntdnynwamgdndsgdnnnaahysganknnwwtgrnnnwykgan 432
                                                                                                                                                                                                  388 TACCTCTGCAACCTAGCAGCACCATGGGGCAGGTGGGACGGCAGCTCGCCATCATCGGGG 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTACCAGCATGGCCTGACTGGCTTCCTAGGCCAGGTGACCCGCTTCGTGGTCG-ACTTCA 684
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                                                  nnnrarndngvnngnsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrr
                                                                                ACG-GCAGAGAATGCCTATGAGTACTTCACCAAGATTGCCACCAGCCTGTTTGAGAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCAAITGGGGCCGTGTGGTGGTCTTCTGGCTTCGGCTACCGTCTGGCCCTACACGT
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (051735). It hybridized to all app. of mycobacteria tested, but cross reacted to a few non-mycobacterial app. The probe may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-Mar-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         970 vgnkmnrycnngdtvnt-asrmnsngnanknhvssttkd 1007
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EP-571911-A.

01-DE-1993.

24-MAY-1993; 108325.

26-MAY-1992; US-889551.

(BECT ) BECTON DICKINSON CO.

Shank DD, Spears PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q51746 standard; cDNA; 91 BP. Q51746;
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WPI; 93-378844/48.
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                                                                                                                                                                                                                                                                                                                                                                                                            E.coll beta-galactosidas rete introduce into the atput ingulation as single stranded template and an oligonucleotide was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which see also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1580 CTCTCCTTATAGACACTTGCTCCCAACCCATTCACTACAGGGTGAAGGCTCTCACCC 1635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUSO) SUOMEN SOKERIO OF CONTROL OF CONTROL OF REINIKAINEN T; (SUSO) SUOMEN SOKERIO OY LECHTOVARAR P. Knowles J, Koivula A, Bamford J, Reinikainen T; WPI: 88-279927/40.

Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elong; mislincorporation, completion of molecules and screening. Disclosure: p: English.

Random point mutations were introduced into the alpha fragment of the sign o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Base substituted E.coll beta-galactosidase alpha-fragment.
E.coll beta galactosidase alpha-fragment; base substitutions;
Escherichia coll.
be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                           Score 43; DB 9; Length yr, Pred; No. 1.89e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 44; DB 1; Length 204; 1.2%; Pred. No. 4.60e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 10
N81164 standard; DNA; 204 BP
                                                                                                                                                                                    Query Match 2.1%;
Best Local Similarity 10.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        larity 11.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-1987; US-034819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1988.
30-MAR-1988; 105163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                            Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure: p; English.

Random point mutations were introduced into the alpha fragment of E-coll beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 C; 17 G; 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nsed for
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                                                                                                                                                                                                                               (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
ss.
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New oligo:nucleotide probes specific for Mycobacteria - used
detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 9; Length 91; Pred. No. 7.69e-11; "...matches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.11e-12;
56; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 1; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 cbnnhvchnvhbnnhrnwayvrhdarrddvhccvch 190
                     /function-multiple cloning site
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Local Similarity 10.48;
les 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.0%;
Similarity 5.8%;
3; Conservative
                                                       187..204
                                                                                                                                        05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
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24-MAY-1993; 108325.
26-MAY-1992; US-889651.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                             WPI; 88-279927/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
EP-571911-A.
                                                                                          /*tag= b
EP-285123-A.
                                                           primer_bind
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Terening a recombinant vector library expressing fusion proteins of the protein and another properties of the proteins of the protein of the proteins of the proteins of the proteins of the proteins of the p
                                                                                                                                                                                                                                                 65-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR, totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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5.5%; Pred. No. 7.46e-08;
vative 32; Mismatches 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Q70465 standard; DNA; 114 BP.
Q70465;
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Q70468;
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(UYNC-) UNIV NORTH CAROLINA.
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PAR 31-77N-1994; US-189331.

PR (UNIV.) UNIV NORTH CAROLINA.

PUR (EVALVES DM. Ray BK;

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                         Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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6, 9 or 12 nucleotides (see
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55..60
(first entry)
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W09418318-A.
18-AUG-1994.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
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                                                                                               129 GGAGATGGAGGTCCGAGGGGTGGTGCTCCTCCTCCAGGGGCTGAGTGGGAGCCCAGT 70
                                    Gaps
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 Score 36; DB 12; Length 114 Pred. No. 2.86e-07; 31; Mismatches 69; Indels
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1.7%;
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070466 standard; DNA; 114 BP.
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15-84R; totally synthetic a ffinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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LID 07
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CRW 75
CW 7
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Terpuis Mobility Moderate and an effector domain a ligand - by screening a recombinant vector library expressing fusion proteins of accenting a recombinant vector library expressing fusion proteins promprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

Disclosure; Page 35; 255pp; English.

CONTAGE is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB) 1(TGC) 2(NNB) 4Z(NNB) 8(TGC) (NNB) CCC 19X; X and Y are flanking restriction sites (X is not the same as Y) CCC 19X; X and Y are flanking restriction sites (X is not the same as Y) CCC 19X; X and Y are flanking restriction sites (X is not the same as Y) CCC are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are peptide between the 2 domains. The oligonoclectides are also designed so that the expressed peptide contains 2 or 4 cysteine residues confer some degree of conformational rigidity to the peptides. The TSARs or compans. comprising a TSAR binding domain can be used in credition or peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. Complex methods of hybridomal antibodies and therefore circumvent the need for complex methods of hybridomal formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing clienter and rapid detection in a screening process.
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Search completed: Thu Aug 21 10:38:25 1997 Job time : 628 secs.

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                                                                                                                                                                                                                                                                                                                                     Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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128:EST128
133:EST133
138:EST133
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173:EST173
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106:EST106
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151:EST151
156:EST156
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yu36g10.rl Homo sapie 0.00e+00

mg88g02.rl Soares mou 0.00e+00

mm518g01.rl Soares mou 0.00e+00

mm518b01.rl Soares mou 0.00e+00

mm50ce01.rl Soares mou 0.87e-35

mm60ce01.rl Soares mou 3.82e-86

KK4771F Homo sapiens 4.39e-67

mm60ce01.rl Soares mou 0.04e-06

yc201.rl Homo sapie 6.17e-06

yc3026.rl Homo sapie 6.17e-06

yc49b08.rl Homo sapie 6.17e-06

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yc49b08.rl Homo sapie 6.17e-06

yc49b08.rl Homo sapie 1.59e-03

H. Sapiens partial cD 1.59e-03

rh Sapiens partial cD 1.59e-03

za21a1.rl Homo sapie 1.59e-03

za21a1.rl Homo sapie 1.59e-03

za21a1.rl Homo sapie 1.59e-03

zb14a04.rl Soares fet 1.59e-03

zb14a04.rl Soares fet 1.59e-03

zb14a04.rl Soares fet 1.59e-03

zb12c08.rl Homo sapie 1.59e-03

zb12c08.rl Homo sapie 1.59e-03

zb12c08.rl Homo sapie 1.59e-03

zb14a04.rl Soares fet 1.59e-03

zb12c08.rl Homo sapie 1.59e-03

zb32c08.rl Homo sapie 1.04e-04

yq6609.rl Homo sapie 1.04e-04
                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  179:EST179
184:EST184
189:EST189
194:EST194
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177:EST177 178:EST178 1
182:EST182 183:EST183 18
187:EST187 188:EST188 1
192:EST192 193:EST193 11
197:EST197 198:EST193 11
                                                                                                                               scale 5.307
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903610.rl Homo sapiens cDNA clone 235938 5'
H52672
9992513
                                                                                                                               Variance 2.224;
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W80365
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175:EST175 176:EST176 1.
180:EST180 181:EST181 18
185:EST185 186:EST186 11
195:EST190 191:EST191 11
195:EST195 196:EST196 11
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H52673
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W23886
AA049828
AA050569
N83998
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AA169681
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            Eukaryozea, Metazoa, Eumetazoa, Bilateria, Coelomata;
Eukaryozeotomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes;
Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes;
Barcopterygil; Choanata, Tetrapoda, Anniota, Mammalia, Theria,
Eutheria, Archonta, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 409)
Hilliar, C., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Holliamson, Y., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stops: 307
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
WashU-warck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watsoo.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 355; DB 84; Length 409;
Pred. No. 0.00e+00;
0; Mismatches 11; Indels 5;
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Matches 390; Conservative
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Bukaryotae; Metazoa; Bumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Butheria; Archorta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 449)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Tan, F., Materston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 339; DB 84; Length 449;
Pred. No. 0.00e+00;
0; Mismatches 13; Indels 11; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WashU-Morck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson wustl.edu
High quality sequence stops: 379
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                       clone=235938 primer=Promega -21ml3 library=Soares ovary tumor
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yu36g10.s1 Homo sapiens cDNA clone 235938 3' H52673
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                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 497)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,M., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
370 taacaaaccaaggtcctaaggccctgtagtttggggcaagggaggagtntaggnagggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Scares mouse embryo NbMEl3.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 484.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
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                                                                                                                            1659 CACTCACCCAAGGCCCC 1643
                                                                                                             430 cattnacccaagggccc 446
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double-stranded CDNA was size selected, ligated to ECO RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 303)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                               ö
                                                                                                                                                                                                                                                                                                                                                                   322 accaogogocccagotgatgccactottaaataggotggaggogatottggtgaagagt 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 tcgtaggcattcccggctgtgggctgaagctgttctagtaaattctggaactctgtgtcg 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 aagaatctgtgtaccacgaattggcccaacagaaccaccaaaaaatcaccattacggtc 141
                                                                                                                                                                                                                                                                            142 aggatggggtetetacgaaaatteagggetgeeacceaecgeetetetgtgegateeat 201
                                                                                                                                      886 ITAAGTCCAGGCAGGGGTCTGAACCGGGACCCAAAGGGCACCCTTGGGAGTCATGATTTG 827
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                                                  Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                               ö
    Length 497;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 bp mRNA EST Homo sapiens cDNA clone 231262 5'.
                                           0; Mismatches 104;
  Score 267; DB 155;
Pred. No. 0.00e+00;
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Query Match 12.8%;
Best Local Similarity 78.1%;
Matches 371; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
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506 ctgttgggt 514
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Soares mouse p3NMF19.5 Mus musculus cDNA clone 329622
SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR BCL-X. ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:211022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           High quality sequence stops: 251
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 gaggagcaggtagcccaggacacagaggaggttttccgcagctacgttttttaccaccat 120
                                                                                                                                                                                                                                                                                                                                                   121 cagcaggaacaggaggctgaaggggcggctgacnc-gacccagagatggtcacctta 179
                                                                                                                                                                                                                                                                                                                                                                                                                 180 cctctgcaacctagcagcaccatggggcaggtgggacggcagctcgccatcattggggac 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 GGGCAAGGCCCAGGTCCTCCCAGGCAGGAGTGCGGAGAGCCTGCCCTGCCCTCTGCTTCT 269
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                                                                                                                                                                                                       Score 266; DB 85; Length 303
Pred. No. 0.00e+00;
0; Mismatches 14; Indels
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tol: 314 286 1800
Email: mouseest@watson.wustl.edu
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                                                                                                      /organism="Homo sapiens"
/clone="231262"
<1..>303
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The WashU-HHMI Mouse EST Project
                                                                             Location/Qualiflers
Email: est@watson.wustl.edu
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                                                                                                                                                                                                     ch 12.7%;
1 Similarity 94.7%;
288; Conservative
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mb16g04.rl 9
similar to 9
W42014
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BASE COUNT
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AUTHORS
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JOURNAL
COMMENT
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AAV49970 446 bp mRNA EST 09-SEP-1996 mj39b01.rl Scares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 478441 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR AAA49970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 ctggcgatgtaatgatgcagtatgatatcagccaaaaagcaggtcacctggcccaggaag 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 tcgtaggcattcccggctgtgggctgaagctgttctagtagattctggaactctgtgtcg 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 aggatggggactctacgaaaattcagggctgccacccaaccgcctctctgtgcgatccat 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 tttagtccagccaggcacgtggctggggccccagtgggtcccc--gggagtcatgatctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             646 CCAGTCAGGCCATGCTGGTAGACGTGTAGGCCCAGAGGCCCAGAAGACCC
                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                Length 545;
Possible reversed clone: similarity on wrong strand Seq primer: EPPrimer EPPrimer High quality sequence stop: 411.

Location/Qualifiers
                                                                                                                                                                                                                                                                  /clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                             Score 248; DB 153; I
Pred. No. 0.00e+00;
0; Mismatches 103;
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                                                           1.545
/organism="Mus musculus"
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Best Local Similarity 77.9%;
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139 c
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US-08-320-157-6.rst

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W23886 161 bp mRNA EST 20-AUG-1996
zb46a10.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 306618
                                                                                                            612 GACGGTAGCCGAAGCCCAGAAGAGCCACCACACCGCCCAATTGATGCCACTCTCAAAAA 553
                                                                                        ggctggaggcgatcttggtgaagagttcgtaggcatttccggctgtgggctgaagctgtt 415
                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 161)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Helman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Watherston,R., Williamson,A., Wohldmann,P. and Wilson,R.. Unpublished (1995)
                        gacggtagccaaagcccaggagagccaccacgcgggccccagctgatgccactcttaaata
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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les 160; Conservative
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AUTHORS
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Marrah M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marrah M., Hucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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Pred. No. 0.00e+00;
0; Mismatches 81; Indels 0
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
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1 Similarity 79.3%;
310; Conservative
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                                     Mus musculus
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house mouse.
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 988 Std Error: 0.00 Seq primer: mob.REG8-tyt. Location/Qualifiers
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Pred. No. 7.70e-255;
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/lab_host-"DH10B (ampicillin resistant)"
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/clone_lib="Soares fetal lung NDHL19W"
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US-08-320-157-6.rst

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Best Local Similarity
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:286320
1063 CCTCCCTCAGCTCTCTGGGACCTCCTTAGCCCTGTCTGCTAGGCGCTGGGGAGACTGATA 1122
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                         AA049828 292 bp mRNA EST 09-SEP-1996 mj09a09.rl Scares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 47576 5'.
AA04928 g1529499
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Pred. No. 3.82e-86;
0; Mismatches 29; Indels
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/dev_stage="13.5-14.5dpc total fetus"
/lab.host="DH10B"
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3.4%;
Best Local Similarity 79.7%;
Matches 137; Conservative
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:286999
                                                                                                                                                                                                                                                                                                                                                         house mouse.
Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                     AAU50569 361 bp mRNA EST 09-SEP-1996 m16b12.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone 476255 5'.
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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/sex="unknown"
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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Pred. No. 3.82e-86;
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                                                                                                                                                                                                                 N83998 232 bp mRNA EST 01-APR-1996
KK4271F Homo sapiens cDNA clone KK4271 5' similar to BAK FOR BCL-2
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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                                                                                             196 ctccaccaagacctgaaaaatggcatctggacaaggaccaggtcccccgaaggtgggctg 255
                                      Molecular Cardiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tal: 4169788758
Fax: 4169785650
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Pred. No. 4.39e-67;
0; Mismatches 1; Indels
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29;
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/clone="KK4271"
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Location/Qualifiers
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Similarity 98.4%;
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Matches 63; Conserv
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
MGI:47664
Seg primer: -28M13 rev2 from Amersham.
                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 ctccaccaagacctgaaaaatggcatctggacaaggaccaggtcccccgaaggtgg-gt- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w//319 445 bp mRNA EST 20-JUN-1996 me64c04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 400326 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 ctgcgatgagtccccgtcc-c-ttctgaacagcaggtgcccaggacacagaggaggt 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 175; Length 270;
Pred. No. 3.69e-38;
0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 76.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 ctttcgaagctac 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 TTTCCGCAGCTAC 314
Mus musculus
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TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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Tat primer=M13 - 21 library=Rat PC-12 cells, untreated vector=pBluescript SK- Rsitel=EcoRI Rsite2=XhoI poly(A)+ RNA was purified from untreated PC12 cells cultured for 9 days. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda 2AP II Vector Kit by Stratagene.
                                                                                                                                       Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3/]; double-stranded CDNA was ligated to Eco El adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco El sites of the modified pT713 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Myomorpha;
Murdae; Murinae; Rattus.
1 (bases 1 to 408)
Lee, M.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A.,
Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D.,
Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:361866
       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 ccgtccccttctgaacagcaggttgcccaggacacagagggtctttcgaagctac
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 186; Length 320
Pred. No. 2.04e-26;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: -28M13 rev2 from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..320 /organism="Mus musculus"
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SET106322 Rattus sp. cDNA 3' end.
H31839
9977256
                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Б
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Best Local Similarity 84.2%;
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                         Waterston, R
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BASE COUNT
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JOURNAL
COMMENT
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                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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/notes
                                                                                            Murinae, Mus.

1 (bases 1 to 445)
Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mr04s013 320 bp mRNA EST 02-DEC-1996 mr04s06.rl Soares mouse 3NbMS Mus musculus cDNA clone 596434 5' similar to TR:G595926 G595926 BAK-2 PROTEIN. ;. AA139013 gg1701240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 tgccttggcggctggactctcagggattctgagcccagagtgagggcagaggtgagatt 325
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@kwatson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares mouse embryo NbME13.5 14.5"
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2.1%; Score 44; DB 126; Length 445;
Best Local Similarity 72.1%; Pred. No. 9.87e-35;
Matchos 80; Conservative 0; Mismatches 30; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 cagaccacagetgtetgaacacatecateaggete-tecaateetgtgtee 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 t
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 341.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex≃"unknown"
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Seg primer: ETPrimer
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1 155 c
                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
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Mus musculus
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KEYWORDS
SOURCE
ORGANISM
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BASE COUNT
ORGANISM
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08-SEP-1995

ACCESSION

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rat primer-M13 Reverse library=Rat PC-12 cells, untreated vector=pBluescript SK- Rsitel=EcoRI Rsite2=XhoI poly(A)+ RNA was purified from untreated PC12 cells cultured for 9 days. cDNA was constructed using an oligo-d7 primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.

1 (bases 1 to 279)
Lee,N.H., Weinstock,K.G., Kirkness,E.F., Earle-Hughes,J.A., Fuldner,R.A., Marmaras,S., Glodek,A., Gooayne,J.D., Adams,M.D., Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
Comparative expressed sequence tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                      ä;
Comparative expressed sequence tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ttgggggcattgcacqtttatttccagacaccgag-ggcgaggtgggggaatccat-ct 64
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For clone availability please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                             the TIGR Database
                                                                                                                                                                                                                                                                                                                                                                                                                      э,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 279;
                                                                                                                                                                                                                                                                                                                                                                                 Length 408;
                                                                                                                                                                                                                                                                                                                          1 others
                                              Jactor Lieaumeur.

Jactor Lieaumeur.

Other_ESTS: EST106323
Contact: Lee NH
The Institute for Genomic Research
932 Clopper Rd, Galthersburg, MD 20878
Tel: 3018699056
Fax: 3018699433
Email: nhleeftigr.org
For clone availability please contact the TIGR Da (tdbinfo@tdb.tigr.org).
                                                                                                                                                                                                                                                                                                                                                                                                                    29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. USA 92, 8303-8307 (1995)
Other_ESTS: EST106322
Contact: Lee NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 82; I
Pred. No. 5.04e-17;
0; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
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SZ1106523 Rattus sp. cDNA 5' end.
H31840
9977257
                                                                                                                                                                                                                                                                               /organism="Rattus sp."
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Fax: 3018699423
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DB

Match Length

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MM114200
AA185611
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MM11158998
AA242472
MM123834
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98 58 56 108

1258 161 133 133 133 133 309 498 498 498 310 320 331 410 410

0.000e+00 1.68e-256 9.33e-256 3.03e-35 3.05e-35 3.05e-35 3.05e-35 1.60e-28 1.60e-28 6.98e-27 6.98e-27 6.98e-27 7.19e-04 7.19e-04 9.94e-03 9.94e-03

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Release 2 Copyright D	1D John F. Collins, Biocomputing Rese (c) 1993, 1994, 1995 University of Estribution rights by IntelliGenetics,
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Run on:	Thu Aug 21 11:29:58 1997; MasPar time 554.19 Seconds 1038.366 Million cell undates/sec
Tabular output no	1
Title: Description:	>US-08-320-157-6 (1-2094) from US08320157.seq
	1 GAGGATCTACAGGGGACAAGCAAAAAAAAAA
Scoring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0; Query 0
Searched:	359085 seqs, 137405154 bases x 2
Post-processing:	
Database: Database:	EST200 3:EST201 4:EST202 5:EST203 6:ES EST206 9:EST207 10:EST208 11:EST209 12 4:EST212 15:EST213 16:EST214 17:EST215 9:EST217 20:EST218 21:EST219 22:EST220 4:EST222 25:EST223 26:EST224 27:EST225 4:EST222 30:EST229 31:EST229 32:EST220 4:EST227 30:EST233 36:EST229 32:EST220 4:EST227 31:EST229 31:EST229 32:EST220 5:TST32 48:ST31 36:ST31 37:ST2 38:EST31 48:ST51 48:ST51 56:GEST3 62:GEST4 63:GEST0 60:GEST1 61:GEST1 61:GEST2 61:GE
Statistics:	Mean 11.796; Variance 2.211; scale 5.335

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AA020955 HS1174584 AA259189

AA018827 G21837

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G06794

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975 sequence; primer; sequence tagged site.

977 sequence; primer; sequences in dbEST and the Unigene collection.

978 sequences in dbEST and the Unigene collection.

978 sequences in dbEST and the Unigene collection.

979 sequences in sequences in dbEST and the Unigene collection.

970 sequences in the Chondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Anniota; Mammalia; Theria; Butheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 9.94e-03 9.94e-03 4.65e-05 4.65e-05 9.94e-03 9.94e-03 Research; Physically 19-0CT-1995 mt62e08.rl Soares 2Nb mt62e08.rl Soares 2Nb zk89a06.rl Soares pre-zk89a06.sl Soares pre-yv67g01.sl Soares fet human STS CHLC.UR_03 yv43f09.sl Soares fet human STS WI-9107. Contact: Thomas Hudson Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research Genome for Whitehead Institute/MIT Center ALIGNMENTS AA185558 AA185558 AA115608 AA115474 N58258 G15924 N53559 DNA ďq G06794 1258 human STS WI-7983. Mapped ESTs Unpublished (1995) 1 (bases Hudson, T. RESULT 1 LOCUS DEFINITION ORGANISM AUTHORS TITLE JOURNAL COMMENT ACCESSION NID REFERENCE KEYWORDS SOURCE

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

& Query

Result

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/organism="Homo sapiens"

281.130

/map="751.A7; 787.E.4; 908.C.6; 923.D.2; 919.D.10;
942.A.12; 808.G.(6,11)"

281.130

/map="751.A7; 787.E.4; 908.C.6; 923.D.2; 919.D.10;
942.A.12; 808.G.(6,11)"

complement(606..625)

/map="751.A7; 787.E.4; 908.C.6; 923.D.2; 919.D.10;
942.A.12; 808.G.(6,11)"

36 a 356 c 335 g 301 t 10 others
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Pred. No. 0.00e+00;
0; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with primer pairs derived from U16811 Location/Qualifiers
Cambridge MA 02142 USA
                                                                                                                                                                                                                                                                                                                                         Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
Taq Polymerase: 0.025 units/ul
                                                                                                    Primer A: CTGATAACTTGGGGAGGCAA
Primer B: GAAGTCCAACTGCAAAGGC
STS size: 345
PCR Profile:
                                                                                                                                                                                                                                      U
                                                                                                                                                                                                              Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                            thudson@genome.wi.mit.
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KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3
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Cambridge Center,
             Tel: 617 252 1900
Fax: 617 252 1902
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                                                                                                                  ctaggacctgagcctggtcctggccgtccctaagcatgtgtcccaggagcaggacctact
                                                                                                                                                1317 CTAGGACCTGAGCCTGGTCCTGGCCGTCCCTAAGCATGTGTCCCAGGAGCAGGACCTACT
                                                                                                                                                                                      gtgggtctatgttccccaggattcagctattctggaagatcagcaccctaagagatggga
                                                                                   GTGGGTCTATGTTCCCCAGGATTCAGCTATTCTGGAAGATCAGCACCCTAAGAGATGGGA
                                                                                                                                                                                                                    1377 AGGAGAGGGGGCCAAGGTCCTGCTCAACTCTACCCCTGCTCCCATTCCTCCTCCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           caggigaaggeteteacecateeetgggggeettggggtgagtggeetgetaaggeteete
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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07-WAR-1997 (Rel. 51, Last updated, Version 2)
2b46a10.rl Soares fetal lung NbHL19W Homo sapiens
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WashU-HHMI Mouse EST Project
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JOURNAL
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                                                                                                                                                                                                         double-stranded cDNA was size selected, ligated to Eco Ri adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library went through one round of
                                                                                                                                                                                                                                                                                                                         normalization to a cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NobHIJ9W."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 acttgggggaggcaagagactgggagccacttctccccagaaagtgtttaacggttttagc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 cctccctcagctctctgggacctccttagccctgtctgctaggcgctgggagactgata 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                 Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL, ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 988 Std Error: 0.00 Seq primer: mob.REGA+ET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91769266
21-FEB-1997 (Rel. 51, Created)
22-FEB-1997 (Rel. 51, Last updated, Version 2)
mt62a08.rl Soares 2NbWT Mus musculus cDNA clone 634454 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN. ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylle T., Lennon G., Soares B., Wilson R.,
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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       Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Tan F., Trevaskis E.,
Waterston R., Williamson A., Wohldmann P., Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 154; DB 88; Length 16 Pred. No. 1.68e-256; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         /clone="306618"
/clone_lib="Soares fetal lung NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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33 A; 46 C; 38 G; 44 T; 0 other;
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MM1142620 standard; RNA; EST; 133 BP.
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Best Local Similarity 99.4%;
Matches 160; Conservative
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by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructedby Bento Soares and M.Fatima Bonaldo."
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.lln.gov) for further information. MGI:386446 Trace considered overall poor quality Possible reversed clone: similarity sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 9.33e-55;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 A; 40 C; 34 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="634454"
/clone_lib="Soares 2NbMT"
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                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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/lab_host="DH10B"
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"The WashU-HHMI Mouse EST Project";
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
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Best Local Similarity 81.6%;
Matches 71; Conservative
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
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Best Local Similarity 81.6%;
Matches 71; Conservative
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA185611 133 bp mRNA EST 07-JAN-1997 mt62a08.rl Soarsa 2NbWT Mus musculus CDNA clone 634454 5' similar to TR:6259206 G595926 BAK-2 PROTEIN. ; ... AA185611 g1769266
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Washington University School of MedicineP 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Fax: 314 286 1810 Email: mousecst@watson.wustl.edu Email: mousecst@watson.wustl.edu This Clone is available royalty.free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:386446
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Pred. No. 9.33e-55;
0; Mismatches 16; Indels
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares 2NbMT"
/sex="male"
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The WashU-HHMI Mouse EST Project
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/dev_stage="4 weeks"
/lab_host="DH10B"
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Best Local Similarity 81.6%;
Matches 71; Conservative
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1 (bases 1 to 309)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marra,M., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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MA21906_rI Soares mouse 3NME12 5 Mus musculus cDNA clone 671386 5/
91842522
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Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                        Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28Mi3 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Pred. No. 9.33e-55;
0; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="634454"
/clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                  /organism="Mus musculus"/strain="C57BL/6J"
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/lab_host="DH10B"
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/organism="Mus musculus"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                              total mouse RNA [providedby Minoru Ko, Wayne State Univ.]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library wen
                                                                                                                                                                                                                                                                                                        through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
/clone="671386" /Clone="150ares mouse 3NME12 5"
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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MX26911.r1 Soares mouse NML Mus musculus cDNA clone 681380 5 .
AA242472
91873149
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91; Length 309;
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: 59 A; 92 C; 91 G; 67 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                           /sex="unknown"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 91;
Pred. No. 3.05e-35;
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          /organism="Mus musculus"
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Best Local Similarity 72.1%;
Matches 80; Conservative
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This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:411090
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20-FEB-1997 (Rel. 51, Created)
20-FEB-1997 (Rel. 51, Last updated, Version 1)
mw21906.rl Soares mouse 3NME12 5 Mus musculus cDNA clone 671386 5'
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Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 3.05e-35;
0; Mismatches 30; Indels
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"The WashU-HHMI Mouse EST Project";
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Best Local Similarity 72.1%;
Matches 80; Conservative
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                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Moris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
Waterston R.,
"The WashU-HHMI Mouse EST Project";
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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11-MAR-1997 (Rel. 51, Last updated, Version 1)
mx26g11.rl Soares mouse NML Mus musculus CDNA clone 681380
                                                                                                                                                                              Score 42; DB 67; Length 498; Pred. No. 7.47e-32;
                                                                                                                                                                                                      0; Mismatches 43; Indels
                                                                       /clone="681380"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH108"
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                                                                                                                                         109
                                                                                                                                                                                                                                                                                                                                                                                                               MM1158998 standard; RNA; EST; 498 BP
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llarity 67.4%;
Conservative
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Best Local Similarity
91; Conserv
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(bases 1 to 310)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Kucaa,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wilson,R. and
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Vertebrata; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae;
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WashU-HIMI Mouse EST Project
WashU-HIMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                      Score 42; DB 92; Length 498;
Pred. No. 7.47e-32;
0; Mismatches 43; Indels
                                                                                                  99 A; 166 C; 124 G; 109 T; 0 other;
                     monse NML"
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Location/Qualifiers
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/sex="male"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                    /tissue_type="Liver"
/lab_host="DH10B"
<1..>498
                 /clone_lib="Soares
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/clone-"681380"
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Local Similarity 67.4%;
les 91; Conservative
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Mus musculus
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/dev_stage="4 weeks"

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                                                                                                      ctccaccaagacctgaaaatggcatctggacaaggaccaggtcccccgaagtgggc-tg 243
                                                                                                                                                   cgatgagtc.-cc-gtcc-c-cttctgaacagcaggttgccaggacacagaggaggt 297
                                                                                                                                                              Gaps
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Key
                                                                                                                                                                                                                                                                                                       25-NOV-1996 (Rel. 50, Created)
19-FEB-1997 (Rel. 51, Last updated, Version 2)
mp93c04.rl Soares 2NDMT Mus musculus cDNA clone 576774 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN, ;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Gelsel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                               7;
                        1 others
                                                        Length 310;
                                                       Score 40; DB 7; Length 310;
Pred. No. 1.60e-28;
0; Mismatches 22; Indels
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                        BP.
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                       standard; RNA; EST; 310
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/lab_host-"DH10B
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                                                      1.9%;
larity 78.2%;
Conservative
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Marram M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marram M., Hillier, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseesf@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:351422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                  7; Gaps
                                                  Length 310;
                                                                                     Indels
                                               Score 40; DB 98; Le
Pred. No. 1.60e-28;
0; Mismatches 22;
mRNA <1..>310
Sequence 310 BP; 72 A; 96 C; 86 G; 55 T; 1 other;
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/strain="C57BL/6J"
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The WashU-HHMI Mouse EST Project
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/lab_host="DH10B"
<1..>310
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                                               Query Match 1.9%;
Best Local Similarity 78.2%;
Matches 104; Conservative
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BASE COUNT ORIGIN

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298

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DEFINITION

ACCESSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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3'); double-stranded cDNA wasligated to Eco RI adaptors (GTTEGATTCGGTACI), dispested with Not I and cloned into t Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
                                                                                                                                    Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LIAL: contact the IMAGE Consortium (info@limage.llnl.gov) for further information. MGI:430469 Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylle T., Lennon G., Soares B., Wilson R.,
                                                                                                                                                                                                                                                           13-FEB-1997 (Rel. 50, Created)
13-FEB-1997 (Rel. 50, Last updated, Version 1)
my25fil.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                  Length 320;
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Pred. No. 6.98e-27;
                                                  Score 39; DB 56; Length 320
Pred. No. 6.98e-27;
0; Mismatches 9; Indels
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/strain="FVB/N"
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Similarity 84.2%;
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Best Local Similarity 84.2%;
Matches 48; Conservative
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Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theishng, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:361866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                            185 ctccaccaagacctgaaaatggcatctggacaaggaccaggtcccccgaagtgggc-tg 243
                                                                                                                                          244 cgatgagtc--ccc-gtcc-c--cttctgaacagcaggttgcccaggacacagaggaggt 297
                                                                                                                                                                                                AA139013 320 bp mRNA EST 16-FEB-1997 mr04e06.rl Scares mouse 3NbMS Mus musculus cDNA clone 596434 similar to TR:G595926 G595926 BAK-2 PROTEIN. ; . g1701240
                                                                                  Gaps
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Pax: 314 286 1810
                                                                                7;
                                                  Length 310
   1 others
                                                Score 40; DB 58; Length 310 Pred. No. 1.60e-28; O; Mismatches 22; Indels
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Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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clone 696909 5'.
AA220617
g1838404
EST.
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WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:430469
                                                                                                                                                                   Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
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/organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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/lab_host="DH10B"
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Ouery Match
1.9%; Score 39; DB 49; Length 331;
Best Local Similarity 84.2%; Pred. No. 6.98e-27;
Matches 48; Conservative 0; Mismatches 9; Indels 0; Gap:
Db 275 ccgtcccttctgaacagcaggttgcccaggacacagaggagttttcgaagctac 331

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QY 258 CCCTCTGCTTCTGAGGAGCAGGTAGCCCAGGACACAGAGGAGTTTTCCGCAGCTAC 314

Search completed: Thu Aug 21 11:52:14 1997 Job time: 1336 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm

Wed Aug 20 10:59:48 1997; MasPar time 5.42 Seconds 445.716 Million cell updates/sec

Tabular output not generated.

>US-08-320-157-7 (1-211) from USO8320157.pep 1561 1 MASGQGPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 211

Perfect Score:

Description:

PAM 150 Scoring table:

Sequence:

96640 segs, 11439865 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

i.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part10 a-geneseq27

Variance 142.854; scale 0.228 Mean 32.533; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

i. No.	5.68e-137	.68e-137	.68e-137	3e-134	7.28e-134	.48e-97	2.53e-90	6.25e-73	1e-14	2.62e-14	te-14	.94e-14	2.48e-13	8e-13	2e-13	3.72e-13	72e-13	72e-13	.72e-13	72e-13
Pred.	5.6	2.0	5.6	7.2	7.2	1.4	2.5	6.2	1.7	2.6	6.8	6,0	2.4	2.4	3.7	3.7	3.7	3.7	3.7	3.7
Description	Bak protein.	Bcl-Y apoptosis-relat			Human Cdn-2.	Human Cdn-1(60-211).	Human Cdn-1(71-211).	Human Cdn-1(96-211).	Chicken lymphoid BCL-	Apoptosis-blocking pr	Human thymus BCL-XL.	Bcl-XL protein.	Apoptosis-blocking pr	Apoptosis-blocking pr	Human bcl-2 beta prot	Human thymus BCL-2.	Human bcl-2 protein.	Human bcl-2 alpha pro	Human oncodene bcl-2	Sequence of bcl-2-alp
QI	W03668	R81451	R77876	W03669	R77877	R77879	R77880	R77881	R68884	W01020	R68887	W05821	W01019	W01018	R71405	R68886	R70332	R71404	R47344	P80987
th DB	11 20	11 17	11 13	11 20	11 13	13	13	116 13	13	19	13	20	19	19	13	13	13	13	239 9	
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Score	1561	1561	1561	1529	1529	1154	1079	868	274	272	266	266	261	261	259	259	259	259	259	259
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3.72e-13 3.72e-13 1.15e-19 2.13e-09 2.13e-09 1.54e-01 1.15e-19 1.1	44
Human bcl-2 protein. Bcl-2 oncogene produc Sequence of bcl-2 bet Apoptosis blocking pr Human Cdn-3. Human mcl-1 gene prod Human mcl-1 gene prod Human thymus BcL-XS. Duffy blood group gpD ACT-4-1 receptor se ACT-4 cell surface re Partial sequence of b Insecticidal protoxin Peripheral nervous sy N. crassa mtr gene pr Mtr protein of Neuros Inositol-3-phosphate Full-length receptor	Full length receptor- Human non-differentia
R70331 P802312 P802312 W001021 W01021 R71407 R77878 R77878 R77878 R77999 R77939 R79955 R79995 R79995 R79995 R79999 R79113 R79163	W06335 R89263
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233 203 203 203 203 192 192 193 277 277 277 471 11157 471 1989 470 2749	987
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0.000000000000000000000000000000000000	86 86
10000000000000000000000000000000000000	44 54 5

ALIGNMENTS

Disclosure; Fig 1; 24pp; English.

Disclosure; Fig 1; 24pp; English.

This Bak protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may brotein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1).

Exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents. Compounds which Human; Bak; apoptosis; latency; virus replication; Epstein-Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; immunoassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic. Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral standard; Protein; 211 AA. 19-APR-1996; U05639, 20-APR-1995; US-426529. (LXRB-) LXR BIOTECHNOLOGY INC. 22-FEB-1997 (first entry) Kiefer MC; Barr PJ, Kiefer M WPI; 96-485886/48. N-PSDB; T42138 Homo sapiens. WO9633416-A1. Bak protein. 24-OCT-1996 protein T W03668

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ö Length 211; Indels Score 1561; DB 20; Pred. No. 5.68e-137; 0; Mismatches 0; Ouery Match 100.0%; Best Local Similarity 100.0%; Matches 211; Conservative

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61 vtlplqpsstmgqvgrqlai1gddinrrydsefqtmlqhlqptaenayeyftkiatslfe 120
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                                                                                                                                                                                                                                                                                                New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig. 3A-B; 66pp; English.

Cdn-1 cDNA was isolated from a human heart cDNA library using a previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HT29 cells. Expression of Cdn-1 in WI-LZ lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 24pp; English.
This Bak-2 protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBW) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may
                                         Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Bak-2; apoptosis; latency; virus replication;
Epstein-Barr Virus; BHRF1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic.
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Pred. No. 5.68e-137;
0; Mismatches 0; Indels 0,
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30-NOV-1993; U2-160067.
07-0CT-1994; US-120157.
(LXRB-) LXR BIOTECHOLOGY INC.
WPI: 95-215106/28.
N-PSDB; Q95492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for anti-viral agents
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20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y match 100.0%; Local Similarity 100.0%; nes 211; Conservative
      (first entry)
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WO9633416-A1.
                                                                                                      Homo sapiens.
W09515084-A.
21-NOV-1995
                    Human Cdn-1
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                                                                               9ginwgrvvallgfgyrlalhvyqhgltgflgqvtrfvvdfmlhhciarwiaqrggwvaa 180
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N-PSDB; T17375.
Now isolated human Bcl-Y protein - used to develop prods. for
treating disorders characterised by inappropriate cell proliferation
or coll death.
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Claim 3: Fig 4: 100pp; English.

Bel-Y protein (R81451) is a member of the Bel-2 family and can had early protein (R81451) is a member of the Bel-2 family and can funduce apoptosis in celis and function as a negative regulator of Bel-2 function. Bel-Y mRNA was detected in all human tumour cell insee examined and is also widely expressed in primary human tissues. It can be obte, by expression of a full-length CDNA clone (T1775) in pref. mammalian host cells. Bel-Y can be used to develop profes, for treating disorders associated with inappropriate cell proliferation or cell death, and to raise antibodies used for the diagnosis or monitoring of such disorders.
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Pred. No. 5.68e-137;
0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                02-JUL-1996 (first entry)
BCl-Y apoptosis-related protein.
BCl-Y; apoptosis; cell proliferation; cell death; diagnosis;
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/label - C-terminal_domain
/note = "putative membrane localisation sequence"
22-per 1.0.
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R77876 standard; Protein; 211 AA.
R77876;
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R81451 standard; Protein; 211 AA
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Local Similarity 100.0%;
nes 211; Conservative
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09-ANG-1995; U10103.
09-ANG-1994; US-287427.
11-OCT-1994; US-321071.
(IMMU.) IMMUNOGEN INC.
Chittenden TD;
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Query Match 73.9%;
Best Local Similarity 100.0%;
Matches 152; Conservative
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WPI; 95-215106/28.
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WPI; 95-215106/
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WO9515084-A.
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R77879 S'
R77879;
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be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak-2 protein and a viral protein (e.g. EBV BRREI), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak-2 and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or
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Cdn-2 cDNA was isold. from a human placental genomic library using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (R77876).

Sequence 211 AA;
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Local Similarity 97.2%; Pred. No. 7.28e-134;
les 205; Conservative 5; Mismatches 1;
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R77877 standard; Protein; 211 AA.
R77877;
21-NOV-1995 (first entry)
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-CCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
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WPI; 95-215106/28.
N-PSDB; 095493.
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WO9515084-A.
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related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly decreased this activity, suggesting that small, truncated Cdn-1 sequence 152 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                 Human Cdn-1(60-211).
Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV, autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences encoding Cdn apoptosis modulators
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Pred. No. 1.48e-97;
0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 lnlgngpilnvlvvlgvvllgqfvvrrffks 211
                                                                                                                                 211
                                                                                                               181 LALGAGPILAVLVVLGVVLLGQFVVRRFFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R77880 standard; Protein; 141 AA.
R77880;
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30-NOV-1993; US-160067.
07-NOY-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                        standard; Protein; 152
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30-NOV-1993; US-160067.
07-COT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC
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Seguence

à 8 ð 요 ò

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New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. neuronal cells, lymphocytes and cancers.

Claim 4: Page 87: 127pp: English.

This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures.

The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 vvngatvhrsslevheivrasdvrgalrdagdefelryrrafsdltsglhitpgtaygsf 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 eqvvnelfhdgvnwgrivaffsfggalcvesvdkemrvlvgrivswmttyltdh-ldpwi 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 VAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYF 111
                                                WPI; 96-427055/43.

Nucleic acids encoding apoptosis regulating proteins - useful for diagnosing and treating immune disorders, malignancies, etc.
diagnosing and treating immune disorders, malignancies, etc.
Example 8; Page 34-35; 60pp; English.

The 80-6 mutant (W01020) of the bcl.-2 oncogene product (W01018) lacks amino acids 80-86 of the native protein. This and other Bcl.-2 mutants (see also W01019-21) were used in a two hybrid assay to examine the interactions between Bcl.-2 and novel apoptosisregulating proteins Nipl, Nip2 and Nip3 (W00997-99). 2 Motifs (W01003-04) on Bcl.-2 were identified that are essential for interaction with the Nip proteins. These motifs show homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W01020;
W01020;
W01020;
18-DEC-1996 (first entry)
Apoptosis-blocking protein Bcl-2 mutant 80-6 (del80-86).
Apoptosis-regulating protein; Bcl-2; oncogene;
adenovirus BlB 19% protein; cell death; cancer; tumour;
immune disorder; diagnosis; therapy; BlplA; Blpl3; Blp5; NIP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 274; DB 13; Length 19
Pred. No. 1.74e-14;
33; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                     Boise LH, Nunez G, Thompson CB; WPI; 95-052079/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.6%;
Best Local Similarity 28.2%;
Matches 37; Conservative
                                   (first entry)
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21-MAR-1995; US-408095.
(UYSL-) UNIV ST LOUIS.
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22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
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172 AQRGGWV-AAL 181
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                                                                                                                                      Gallus domesticus.
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                                                                                                                                                          WO9500642-A.
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                                                                                                                                                                                05-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                             71 MGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIATSLFESGINWGRVVA 130
                                                                                                                                                                                                                                                                                                                                            mgqvgrqlaligddinrrydsefqtmlqhlqptaenayeyftkiatslfesginwgrvva 60
New nucleic acid sequences encoding cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                   Disclosure; Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 70 amino acids of Cdn-1 improved this activity, suggesting that small, truncated Cdn-1 molecules may be potent therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in Tarcassed cell survival in response to anti-Fas-mediated apoptosis. Iruncated Cdn-1 derivatives given in R77879-81 were used to test the effects of deleting the N-terminal sequences of Cdn-1 on this activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 rfvvdfmlhhciarwiaqrggwvaalnlgngpilnvlvvlgvvllgqfvvrrffks 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Cdn-1(96-211).

Human Cdn-1(96-211).

Gdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.

Homo sapiens.

W09515084-A.

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                                                                                                                                                                                                                                                          Score 1079; DB 13; Length 141;
Pred. No. 2.53e-90;
0; Mismatches 0; Indels 0
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Pred. No. 6.25e-73;
0; Mismatches 0; Indels
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30-NOV-1993; US-160067.
07-CCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 VLVVLGVVLLGQFVVRRFFKS 211
                                                                                                                                                                                                                                                          Query Match
Bost Local Similarity 100.0%;
Matches 141; Conservative
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Best Local Similarity 100.0%;
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WPI; 95-215106/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 AA;
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Sequence

NATURE SULTANDE SULTA

Matches

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2; Gaps

Length 190

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Matches

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Inducting or preventing death of T cells by bcl-XL protein regulation

Tursdup, increase survival of HIV infected cells or to

Gown:regulate immune responses in immune diseases

Disclosure; Page 52-53; 76pp; English.

This is the sequence of a human bcl.XL protein, which protects

T-lymphocytes against cell death. A splice variant form, bcl-XS,

acks a stretch of 63 amino acids, and is a dominant negative

regulator of bcl-XL function. The gene may be modified to

facilitate interaction with costimulatory Bax protein and inhibit

interaction with antagonistic Bad protein, by modification of the

Bcl-2 homology domains BHI and/or BH2. The bcl-XL gene may be

introduced into T-cells in vivo or ex vivo via gene transfer using

a vector for HIV infection gene therapy, to augment intracellular

bcl-XL protein levels and protect from cell death. A corresponding

antisense oligonuclectide or expression vector may be used in gene

therapy of e.g. autoimmune disease, graft rejection or graft-

corresponding in the interaction of the corresponding interaction or graft-

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therapy of e.g. autoimmune disease, graft rejection or graft-

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Human; bc1-XL; T-1ymphocyte; cell death; BH1 domain; BH2 domain;
BC1-Z homology domain; gene therapy; HIV; AIDS; antisense;
immune discorder; autoimmune disease; graft rejection;
graft-versus-host disease; apoptosis; adoptive immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             down-regulate the immune response in a T-lymphocyte population
Sequence 233 AA;
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Pred. No. 8.94e-14;
42; Mismatches 60;
                                                                                                                                                                                                                  Location/Qualifiers
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25.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-1996; U06203.
04-MAY-1995; US-435518.
07-JUN-1995; US-481739.
(ARCH-) ARCH DEV CORP.
(USNA ) US SEC OF NAVY.
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(UYSL-) UNIV ST LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thompson CB;
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21-MAR-1996; 104542.
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                                                                                                                                                                                                                                                                                                                                             "BH2 domain"
                                                                                                                                                                                                                                                                                   /note= "BH1 domain
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WPI; 96-506159/50.
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                                                                                                                                                                                 Homo sapiens.
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WPI: 95-052079/07.

N-PSDB: 091698.

New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. antibodies, useful in assay and cancers.

Claim 3: Page 94: 127pp; English.

C This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures. The programmed cell death (PCD)) or neurodegenerative and autoimmune classes (premature PCD), e.g. Parkinson's disease, amylotrophic lateral sclerosis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   optosis; cell death; cancer; neurodegenerative disease; disease; Parkinson disease; amylotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                            48 ffssqpghtphp-aasrdpvartsplqtpaapgspvppvvhlt1rqagddfsrryrrdfa 106
                                                                                                                                                                                                                                                                                                                                                                                                          107 emssqlhltpftargcfatvveelfrdgvnwgrivaffefggvmcvesvnremsplvdni 166 | :|: |: || ||: || ||: :|: :: :: :|
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                              .;
8
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Pred. No. 8.94e-14;
42; Mismatches 60; Indels 3
to motifs (W01005-06) identified on the adenovirus EIB 19K apoptosis-blocking protein (W01010).
                                                                                                                                         Length 232
                                                                                                                                  Score 272; DB 19;
Pred. No. 2.62e-14;
41; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : ::::: | : | | : | | | :: | | : | | 155 TRFVVDFMLHHCIARWIAQRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 alwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 11
R68887 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W05821 standard; Protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL-XL; apoptosis; cell death;
autoimmune disease; Parkinson d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 epwiqenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 ARWIAQRGGWVAALNL-GNGP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 17.0%;
Best Local Similarity 25.5%;
Matches 36; Conservative
                                                                                                                                  17.4%;
Local Similarity 29.7%;
Les 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W05821;
30-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human thymus BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multiple sclerosis
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WO9500642-A.
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                                                                    Seguence
                                                                                                                                         Query Match
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RESULT ID W0 AC W0 DT 30

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Gaps

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Length 233;

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Query Match
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                                                                    diagnosing and treating improcess required.

Example 8; Page 33-14; GOpp: English.

The 42-8 mutant (W01019) of the bcl-2 oncogene product (W01018)

1acks amino acids 42-48 of the native protein. This and other

1acks amino acids 42-48 of the native protein. This and other

1bcl-2 mutants (see also W01020-21) were used in a two hybrid assay

1c examine the interactions between Bcl-2 and novel apoptosis-

1c equiating proteins Wipl, Wip2 and Nip3 (W00997-99). The Nip

1c proteins were unable to interact with mutant 42-8. The site of

1c deletion in this mutant corresponds to a motif (see also W01003)

1c show homology to motifs (W01004) of Bcl-2 was also identified, and both

1c wollow) of adenovirus ElB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-1996.
21-MAR-1996.
21-MAR-1996.
31-MAR-1996.
32-SEP-1996.
33-SEP-1996.
34-SEP-1996.
35-SEP-1996.
36-SEP-1996.
36-SEP-1996.
37-SEP-1996.
38-SEP-1996.
39-SEP-1996.
39-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 APADPEMVTLP-LOPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 tvv60lfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargcfa 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps

    useful for

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Apoptosis-blocking protein Bcl-2.
Apoptosis-regulating protein, Bcl-2; oncogene;
ademovirus ElB 19K protein; cell death; cancer; tumour;
immune disorder; diagnosis; therapy; Bipla; Bipl3; Bip5; NIp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 261; DB 19; Length 232;
Pred. No. 2.48e-13;
37; Mismatches 57; Indels
                                                            proteins
Chinnadural G;
WPI; 96-427055/43.
Nucleic acids encoding apoptosis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding_site 43.51
/labbl_Binding_motif
/note= "interacts with Bip proteins"
Binding_site 106.112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Binding_motif
/note= "interacts with Bip proteins"
EP-733706-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W01018 standard; Protein; 239 AA. W01018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 QRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 dnggwdafvel-ygpsmrpl 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 16.7%;
Local Similarity 29.3%;
Nes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Wethods for producing and identifying mutant bcl-2 proteins -
Methods for producing and identifying mutant bcl-2 proteins -
that lack death repressor activity and/or lacks binding to Bax.

By Disclosure; Page 40; 133pp; English.

The sequences given in R71404-05 represent the human bcl-2 alpha and
beta proteins respectively. bcl-2 is encoded by a proto-oncogene and
compares in hibiting apoptosis in many hematopoletic cell systems.
bcl-2 is a 26 kD membrane-associated cytoplasmic protein and is thought
co function by enhancing the survival of hematopoletic cells of B and T
corigins rather than directly promoting proliferation of these cell
corigins rather than directly promoting proliferation of these cell
corigins rather than directly promoting proliferation of these cell
corigins rather than directly promoting proliferation of these cell
corigins rather than directly promoting proliferation of these cell
corigins rather than directly promoting proliferation of these cell
corigins rather than directly promoting an epopence
concentrations of IL-3. bcl-2 has been shown to form hererodiners with
concentrations of IL-3. bcl-2 has been shown to form hererodiners with
concentrations of IL-3. bcl-2 has been shown to form hererodiners with
concentrations of IL-3. bcl-2 has been shown to form hererodiners with
concentrations of IL-3 bcl-2 and Bax determines cell survival or death
collowing an apoptotic stimulus. The invention gives a mutant form
collowing an apoptotic stimulus. The invention acid substitution or deletion
in the BHI or BH2 domains. This makes the mutant protein substantially
concentration of bcl-2 is useful in cancer therapy, controlling
concentration death effector molecules. Up regulating bcl-21s beneficial in
treatment and diagnosis of immunodeficiency diseases, including AIDS and
concentrative and ischaemic cell death.
                                                                                                                                                                                    132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190
                                                                                          74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargcfa 131
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis; membrane-associated cytoplasmic protein; B cell; T cell; proliferation; cell cycle progression; Bax; apoptotic cell death; poptosis; cytokine; death repressor; BH1; BH2; cancer therapy; hyperplasia; immunodeficiency disease; AIDS; neurodegeneration; ischaemic cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-007-1995 (first entry)
Human bcl-2 beta protein.
Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
                                                    ų,
         Length 239;
    Score 261; DB 19; Length 23
Pred. No. 2.48e-13;
37; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Represents Bax binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Represents Bax binding site"
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136..155
                                                                                                                                                                                                                                                                                                                                                                                           T 15
R71405 standard; protein; 205 AA.
R71405;
                                                                                                                                                                                                                                                                           191 dnggwdafvel-ygpsmrpl 209
                                                                                                                                                                                                                                                                                                        : ||| | ::| || : |
173 QRGGWVAALNLGNGPILNVL 192
Query Match
Best Local Similarity 29.3%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U09701.
US-112208.
US-248819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1994;
26-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9505750-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
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Length 205;

Score 259; DB 13; Pred. No. 3.72e-13;

16.6%;

Best Local Similarity

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Matches 38; Conservative 37; Mismatches 49; Indels 4; Gaps 3;

Db 74 tpaapgaaagpalspypvvhla--lrqagddfsrryrgdfaemssqlhltpftargrfa 131

Qy 54 APADPEMYTLP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFGTMLQHLQPTAENAYEYFT 112

Db 132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdnialwmteylnrh-lhtwiq 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdnialwmteylnrh-lhtwig 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwig 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwig 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwig 190

113 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwid 190

114 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwid 190

115 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwid 190

115 tlyveelfrdgvnwgrivaffefgrmcvesvnremsplvdialwmteylnrh-lhtwid 190

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115 tlyveelfrdgvnwgrmcvesvnremsplvdialwmteylnrh-lhtwid 190

115 tlyveelfrdgvnwgrmcvesvnremsplvdialwmteylnrh-lh
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Aug 20 11:00:51 1997; MasPar time 8.88 Seconds 686.301 Million cell updates/sec Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-08-320-157-7 (1-211) from USO8320157.pep 1561 1 MASGGGFGPPRQECGEPALF.....LVVLGVVLLGGFVVRRFFKS 211

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues Searched:

Post-processing:

Database:

Minimum Match 0% Listing first 45 summaries

pir51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Mean 45.149; Variance 108.206; scale 0.417 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Core Match Length DB 1D Description Pred. No. 1561 100.0 211 13 558873 Bak protein - human 4.94e-244 17.6 190 13 558875 apoptosis regulator 3.11e-24 270 17.3 233 14 551761 BCL-X protein - huma 2.15e-23 270 17.3 233 14 149056 bcl-x protein - huma 2.15e-23 270 17.3 233 14 149056 bcl-x long - mouse 1.27e-23 26 17.0 233 18 47537 apoptosis regulator 5.19e-22 26 17.0 233 14 149057 bcl-x long - mouse 1.27e-23 26 16.8 216 6 137332 transforming protein 2.19e-22 25 16.3 239 2 TVHUB1 transforming protein 2.99e-22 16.3 206 6 D37332 transforming protein 2.43e-21 25 16.3 239 2 TVHUB1 transforming protein 1.38e-20 25 16.0 236 2 TVMSB1 transforming protein 1.38e-20 27 27 27 27 27 27 27 27 27 27 27 27 27			æ			SUMMARIES		
100.0 211 13 \$58875 Gn-2 protein - human 98.0 211 13 \$58875 Gn-2 protein - human 2.17.6 190 13 A47537 apoptosis regulator 3.17.3 233 14 \$51761 BCL-X protein - rat 1.7.3 233 14 \$51761 BCL-X protein - rat 1.7.0 233 13 B47537 apoptosis regulator 5.16.8 216 6 B37332 transforming protein 2.16.7 233 6 A37332 transforming protein 2.16.1 233 14 \$16737 \$16.0 \$1	Score	-	Quer		DB	OI.	Description	
98.0 211 13 558875 cdn-2 protein - huma 2. 17.6 190 13 A47537 apoptosis regulator 3. 17.3 233 14 551761 BCL-x protein - rat 17.3 233 14 149056 bcl-x long - mouse 17.0 233 13 B47537 apoptosis regulator 5. 16.8 216 6 B37332 transforming protein 5. 16.7 233 6 A37332 transforming protein 2. 16.3 206 6 D37332 transforming protein 2. 16.3 239 2 TVHUM1 transforming protein 2. 16.0 199 2 TVMSM1 transforming protein 1. 16.0 236 4 167432 transforming protein 1. 15.3 232 6 524390 transforming protein 1. 15.3 232 6 524390 transforming protein 1. 15.3 232 8 524390 transforming protein 6. 13.9 192 13 A47538 bcl-2-associated pro 2. 18.13 B47538	156	۱,-	100.	0 211	13	S58873	Bak protein - human	4.946-244
17.6 190 13 A47537 apoptosis regulator 17.3 233 4 \$51761 BCL-X protein - rat 17.3 233 4 \$51761 BCL-X protein - rat 17.0 233 13 4 149056 bcl-x long - mouse 16.8 214 4 149057 bcl-x transmembrane 16.8 216 6 B37332 transforming protein 216.5 205 2 TVHUB1 transforming protein 216.3 239 2 TVHUB1 transforming protein 216.3 239 2 TVHUB1 transforming protein 239 2 TVHUB1 transforming protein 216.0 236 2 TVHUB1 transforming protein 216.0 236 2 TVMSA1 transforming protein 216.0 236 2 TVMSA1 transforming protein 236 2 2 2 2 2 2 2 2 2	152	ō.	98.	0 211	13	S58875	cdn-2 protein - huma	2.15e-238
17.3 233 14 551761 BCL-X protein - rat 1.7.3 233 14 149056 bcl-x long - mouse 1.7.3 233 13 140556 bcl-x tong - mouse 1.6.8 214 14 149057 apoptosis regulator 5.16.8 216 6 B37332 transforming protein 2.16.7 233 6 A37332 transforming protein 2.16.3 206 6 D37332 transforming protein 2.16.3 206 6 D37332 transforming protein 2.16.3 239 2 TVHUBA1 transforming protein 2.16.1 233 14 167431 BCL-X-Long - rat 6.16.0 236 2 TVMSB1 transforming protein 1.16.0 236 2 TVMSB1 transforming protein 1.16.0 236 14 167432 transforming protein 1.16.0 237 6 B37332 transforming protein 1.16.3 232 6 S24390 transforming protein 6.13.9 192 14 D47538 bcl-2-associated pro 4.13.9 218 13 B47538 bcl-2-associated pro 4.	7	74	17.	6 190	٦	A47537	apoptosis regulator	3.11e-24
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#gene GDB:BAK-LSB ##cross-references GDB:635887 SUMMARY #length 211 #molecular-weight 23409 #checksum 801

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##status preliminary
##molecule_type mRNA
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Nature (1995) 374:736-739
Modulation of apoptosis by the widely distributed Bcl-2
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Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
C.B.
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bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.
A47537
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BCL-X protein - rat
#formal_name Rattus norvegicus #common_name Norway rat
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Pred. No. 1.27e-23;
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Best Local Similarity 28.2%; Pred. No. 3.11e-24;
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17.3%;
Best Local Similarity 25.5%;
Matches 36; Conservative
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S51761; S51762
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##residues 1-1
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Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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                                                                                                                                                                                                                                                                                                 #authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in and T lymphocytes.
#cross-references MUID:95052604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 EAEGVAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENA 107
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                                                                            bcl-x long - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
15-Oct-1996
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16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
06-Sep-1996
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Pred. No. 1.27e-23;
42; Mismatches 60; Indels 3;
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##molecule_type mRNA
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apoptosis regulator bcl-xL - human
bcl-2-related protein
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##cross-references GB:L20121; CDS_PID:Q07817
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                                                    *type complete
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Best Local Similarity 25.5%;
Matches 36; Conservative
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I49055
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*product apoptosis regulator bcl-xs *status predicted *label MA2
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bcl-x transmembrane deleted - mouse
#formal_name Mus musculus *common_name house mouse
02.Jul-1996 *sequence_revision 02-Jul-1996 *text_change
149057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 153:4388 4398
#title Cloning and molecular characterization of mouse bcl-x and T lymphocytes.
#cross-references WIID:95052604
#accession I49057
                                                                                                                                                                                                                          #molecular-weight 26063 #checksum 5340
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##cross-references EMBL:U10102; NID:9506649; CDS_PID:9506650
                                                                                                                                                 #product apoptosis regulator bcl-xL #status
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                                                                                                                                                                                                                                                                                                   42; Mismatches 60; Indels
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                   B02
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#length 214 #molecular-weight 23900
               ##residues 1-69,'G',71-125,189-233 ##label ##cross-references GB:L20122; CDS_PID:9623237
                                                                                                                                                                                                                                                             Score 266; DB 13;
Pred. No. 5.19e-23;
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                                                                                      ##cross-references GDB:228079
ADS alternative splicing; apoptosis
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Best Local Similarity 25.5%;
Matches 36; Conservative
                                                                                                                                                                                                                        #length 233
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##residues 1-214
##molecule_type mRNA
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Nucleic Acids Res. (1992) 20:4187-4192
Scalation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
                                                                                           Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Notleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A37332 *type complete
transforming protein (bcl-2-alpha) - chicken
*formal_name Gallus gallus *common_name chicken
03-Mar-1993 *sequence_revision 03-Mar-1993 *text_change
12-Apr-1995
A37332; S35453
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#formal_name Gallus gallus #common_name chicken
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                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 216;
                                                                                                                                                                                                                                                                                                                                                                    Score 262; DB 6; Length 216
Pred. No. 2.11e-22;
38; Mismatches 56; Indels
                                                                                                                                                                          neuronal organs in adult and embryo.
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transforming protein
*length 233 *molecular-weight 25687
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Best Local Similarity 28.5%;
Matches 39; Conservative
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#authors Tsujimoto, Y.; Croce, C.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products
of bcl-2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
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#map_position 18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q21.33-18q2
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Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
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                                                                                                                                                                       TVHUB1 *type complete transforming protein bcl-2-beta - human *formal_name Homo sapiens *common_name man 31-bec-1988 *sequence_revision 31-bec-1988 *text_change 06-sep-1996
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#superfamily bcl transforming protein
#length 206 #molecular-weight 22440 #checksum 5581
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Pred. No. 2.43e-21;
35; Mismatches 51; Indels
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##residues 1-205 ##label TSU
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#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products
#cross-references MUID:86259760
#accession A29409
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#journal EMBO J. (1988) 7:123-131
#title Alternative promoters and exons, somatic mutation and derequiation of the Bcl-2--Ig fusion gene in lymphoma.
#cross_references MUID:88196071
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#journal Cell (1986) 47:19-28
#title Cloning and structural analysis of cDNAs for bcl-2 and a
hybrid bcl-2/immunoglobulin transcript resulting from the
(14:18) translocation.
#cross-references MUID:87002488
                                                                                                                                                                                                                                                                                                                                                                      Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20.4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A. Wright, J.J.; Bakhshi, A. Bakhshi, A. Bakhshi, A. Bakhshi, A. Choogene Res. (19188) 2:263-275 atitle Consequences of the t(14:18) chromosomal translocation in follicular lymphoma: deregulated expression of a chimeric and mutated BCL-2 gene.
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this sequence has been corrected in reference A37332
                                                           54 APADPEMVILP-LQPSSIMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT 112
                                      133 twveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 191
                                                                                                                                                                                                                                                    transforming protein bol-2, splice form alpha - human #formal_name Homo sapiens #common_name man 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequence not shown; not compared with conceptual translation
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##realdues 1-58,'T',60-116,'R',118-239 ##label
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Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology (1995) 136:232-241

Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
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#superfamily bcl transforming protein
alternative splicing; B-cell lymphoma; follicular lymphoma;
proto-oncogene; transforming protein
#length 239 #molecular weight 26266 #checksum 8323
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sidues 1-6,'S',8-58,'T',60-128,'C',130-239 ##label HUA2 te the sequence was determined from the germine gene constitutive expression of BCL2 following t(14:18) chromosomal translocation is typically found in follicular lymphoma.
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transforming protein bol-2-beta - mouse
fromal_name Mus musculus #common_name house mouse
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
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Pred. No. 6.88e-21;
31; Mismatches 50; Indels
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Pred. No. 2.43e-21;
37; Mismatches 57;
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#map_position 18q21.33-18q21.33
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#journal Cell (1987) 49:455-463
#title Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.
#cross-references MUID:87187643
#accession A25960
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Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
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transforming protein bcl-2-alpha - mouse
transforming protein bcl-2-alpha - mouse
#formal_name Mus musculus *common_name house mouse
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#title Molecular analysis of mbcl-2: structure and expression murine gene homologous to the human gene involved in follicular lymphoma.
#cross-references MUID:87187643
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Matches 32; Conservative
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Aug 20 11:01:54 1997; MasPar time 6.20 Seconds 722.269 Million cell updates/sec Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-08-320-157-7 (1-211) from USO8320157.pep 1561 1 MASGQGPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 211

PAM 150 Gap 11 Scoring table:

59021 segs, 21210388 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Database:

Mean 47.042; Variance 90.697; scale 0.519 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.		
Pred. 1	3.4.5e-29 9.4.6e-29 1.2.4e-26 1.0.2.4e-26 1.0.2.4e-26 1.0.2.4e-26 1.0.2.4e-26 1.0.2.4e-26 1.0.2.4e-26 1.0.2.4e-17	
Description	APOPTOSIS REGULATOR B APOPTOSIS REGULATOR B APOPTOSIS REGULATOR B APOPTOSIS REGULATOR B PROTEIN BCL-2-BETA. PROTEIN BCL-2-BETA. PROTEIN BCL-2-ALPHA. PROTEIN BCL-2 ALPHA. PROTEIN BCL-2 ALPHA. APOPTOSIS REGULATOR B APOPTOS	
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Length DB	190 2333 20333 205 236 236 236 236 192 192 193 173 173 173 173 173 173 173 173 173 17	
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Score	274 260 261 261 261 261 261 261 261 261 261 261	
Result No.	11111111111111111111111111111111111111	

233 AA.

PRT;

STANDARD;

RESULT 2 ID BCLX_RAT

567 5 HXT3_YEAST LOW-AFFINITY GLUCOSE 4.58e-01 814 4 GUNE_CLOTM ENDOGLUCANASE B PRECU 1.09e+00 206 7 PEMZ_YEAST METHYLEME_FATTY_ACKL_1.22e+00 569 5 HXT8_YEAST HEXOSE TRANSPORTER HX 1.92e+00 817 8 RRPO_TBSVC 818 1 ART6_SCHPO HYPOTHETICAL 59.6 KD 1.92e+00 818 1 ART6_SCHPO ARC11 PROTEIN PRECURS 1.92e+00 531 11 YP60_METTH HYPOTHETICAL 60.5 KD 2.54e+00 531 11 YP60_METTH HYPOTHETICAL 60.5 KD 2.54e+00 833 3 CMAL_YEAST PROTEIN WHALI PRECURS 3.55e+00 196 6 MORA_PSEPU MORPHINE 6-DEHYDROGEN 7.57e+00 294 6 MORA_PSEPU MORPHINE 6-DEHYDROGEN 7.57e+00 567 5 HXT8_YEAST HEXOSE TRANSPORTER HX 7.57e+00 567 5 HXT8_YEAST HEXOSE TRANSPORTER HX 7.57e+00 567 5 HXT8_YEAST HIGH AFFINITY HEXOSE 7.57e+00 568 8 PYFE MYCG PRESURE HX 7.57e+00 569 8 HYFE MYCG PRESURE HX 7.57e+00 822 11 YJC9_YEAST HYPOTHETICAL 95.4 KD 5.78e+00 1103 8 RPOBE_CYAPA DNA_DIRECTED RNA POLY 7.57e+00 412 11 YAA7_SCHPO HYPOTHETICAL 45.7 KD 5.78e+00 412 11 YAA7_SCHPO HYPOTHETICAL 45.7 KD 9.89e+00 441 1 AROA_PASMU 3-PHOCHHETICAL 45.7 KD 9.89e+00 441 1 AROA_PASMU 3-PHOCHHETICAL 45.7 KD 9.89e+00 441 1 AROA_PASMU 3-PHOCHHETICAL 45.7 KD 9.89e+00 442 9 TISD_HUMAN TISIID PROTEIN (EGF-R 9.89e+00		
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233 AA;
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A BOISE LH., GONZALEZ-CARCIA M., POSTEMA C.E., DING L.,
A BOISE LH., GONZALEZ-CARCIA M., POSTEMA C.E., DING L.,
BOISE LH., GONZALEZ-CARCIA M., POSTEMA C.E., DING L.,
CELL 74:597-608(1993).
- I- FUNCTION: DOWINANT REGULATOR OF APOPTOTIC CELL DEATH.
- I- FUNCTION: DOWINANT REGULATOR OF APOPTOTIC CELL DEATH.
- I- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
- I- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
- I- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
- I- THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
- LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
- I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

REMBL: Z23115; G510901; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-BRAIN;

TISSUE-BRAIN;

SUBMITTED (DEC-194) TO EMBL/GENBANK/DDBJ DATA BANKS.

SUBMITTED (DEC-194) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I - FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.

-I - ALTERNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE) AND BCL-X(S), ARE DERIVED BY ALTERNATIVE SPLICING.

-I - SIMILARIY: BELONGY TO THE BCL-2 FAMILY.

EMBL; X82537; G607177; --

EMBL; X82537; G607178; --

APOPTOSIS; ALTERNATIVE SPLICING.

MISSING (IN BCL-X(S)).
                                                                                                                                                                                                                                                       RATTUS NORVEGICUS (RAT).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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G -> A (IN G510901).
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233 AA; 26130 MW; E0589815 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 270; DB 1; I
Pred. No. 1.95e-29;
42; Mismatches 60;
                                   01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-X.
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APOPTOSIS; ALTERNATYE SPLICING.
126 188 MIS
CONFLICT 70 G G
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168 ARWIAQRGGWVAALNL-GNGP 187
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Bost Local Similarity 25.5%;
Matches 36; Conservative
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Q07817;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 hhrpeppgsaaasevppae-glrpapp-g-vhlalrqagdefsrryqrdfaqmsgqlhlt 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 pftahgrfvavveelfrdgvnwgrivaffefggvmcvesvnremsplvdniatwmteyln 176
                                                                                                                                           120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndh-1 178
                                                                                                                                                               61 dspavngatghs-ssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgta 119
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
E -> S (IN REF. 2).
GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                       .;
`
17.0%; Score 266; DB 1; Length 233; 25.5%; Pred. No. 1.10e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 261; DB 1; Length 233
Pred. No. 9.46e-28;
41; Mismatches 57; Indels
                                       Indels
                                   42; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IN REF. 2).
H -> T (IN REF. 2).
G -> V (IN REF. 2).
4; 3376502C CRC32;
                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                               233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, S24390; S24390.
PROSITE; PS01080; BCL2.
APOPIOSIS; TRANSMEMBRANE; MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE, 92375724.
MEDLINE, 92375724.
MUCHIT Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992)
                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                    epwigenggwdtfvelygnna 199
                                                                                                                                                                                                                                                      168 ARWIAQRGGWVAALNL-GNGP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D11381; G222794; -. EMBL; D11381; G222794; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25687 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.5%;
Matches 41; Conservative
                25.5%;
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      APOPTOSIS REGULATOR BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 211961; G62970; -.
                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GALLUS GALLUS (CHICKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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PIR; S24390; S24390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 AA;
                Best Local Similarity
Matches 36; Conser
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**SUBCELLULAR LOCATION.

**AEDLINE; 91066924.

A HOCKERBER D., WINDEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;

**NATURE 348:334-336(1990).

C -1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT SUCH AS MITOCHONDRIA.

C -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

C -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.

C -1- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMSGOMAL TRANSLOCATION

C -1- DISEASE: MHICH INVOLVES BCLZ AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.3%; Score 255; DB 1; Length 205; Best Local Similarity 29.7%; Pred. No. 1.24e-26; Matches 38; Conservative 35; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 86259760
TSUJIMOTO Y. CROCE C.M.;
PROC. NATE. ACAD. SCI. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                  01-MAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTEIN BCL-2-BETA.
                                                                                                                                         205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992)
                                             177 rh-lhnwigdnggwdafvelygns 199
:|: ||: ||: ||:
164 HHCIARWIAQRGGWVAALNL-GNG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M13995; G179369; ALT_SEQ.
PIR; B29409; TVHUB1.
PIR; D37332; D37332.
MIM; 151430; -.
                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS TO 96 AND 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 QRGGWVAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 dnggwvga 198
                                                                                                                      LT 5
BC2B_HUMAN
P10416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGIONS
                                                                                                                      8
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-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
TICHIGO (032;021) WHICH INVOLVES BCLZ AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOCKENBERY D., NUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
NATURE 348:334-336(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; MI394; GI79367; ALT_SEQ.
EMBL; MI4745; G179371; -.
PIR; A29409; TVHUA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01080; BCL2.
PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE;
MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 239;
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Pred. No. 1.24e-26;
37; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P -> T (IN REF. 3).
S -> R (IN REF. 3).
75084859 CRC32;
                                                                               01-MAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEARY M.L., SMITH S.D., SKLAR J.;
CELL 47:19-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 PC
59 P
117 S
; 26266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO 96; 110 AND 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.3%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 86259760. TSUJIMOTO Y., CROCE C.M.;
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION.
                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN)
                                                                                                                                                                        PROTEIN BCL-2-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A24428; TVHUBC.
PIR; C37332; C37332.
MIM; 151430; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87002488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 91066924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
LT 6
BC2A_HUMAN
P10415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
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   RESULT
                                                             SOTT THE TRANSPORT OF THE PROPERTY OF THE PROP
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TISSUE-BRAIN
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BCL2_RAT
P49950;
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
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                                                                                                                                                                                                                                                                                                                                                      NEGRINI M., SILINI E., KOZAK C., TSUJIMOTO Y., CROCE C.M.; CELL 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/C; TISSUE-LIVER;
MEDLINE; 87187643.
NEGRINI M., SILINI E., KOZAK C., TSUJIMOTO Y., CROCE C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 250; DB 1; Length 199;
Pred. No. 1.05e-25;
29; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwvga 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 LALHVYQHGLIGFLGQVIRFVVDFMLHHCIARWIAQRGGWVAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SULT 8
BC2A_MOUSE STANDARW,
P10417;
T 01-MAR-1989 (REL. 10, CREATED)
JT 01-SPR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PROTEIN BCL-2 ALPHA.
BCL2 OR BCL-2.
BCL2 OR BCL-2.
                                                                                                BC2B_MOUSE STANDARD; PRT; 199 AA.
P10418;
01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTEIN BCL-2-BETA.
BCL2 OR BCL-2.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS TO 221-222.
MEDLINE, 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
              191 dnggwdafvel-ygpsmrpl 209
                                   : || | :: | || : |
173 QRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 31.1%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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NUCLEIC ACIDS RES. 20:4187-4192(1992).

- 1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF FREQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF PREE RADICAL GENERATION SUCH AS MITOCHONDRIAL.

-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

-1- SISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.

-1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.

-1- SIMILARITY: BELONGS TO THE BCL-2: FAMILY.

REMBL; LA15132; G387109; JOINED.

REMBL; LA1532; G387109; JOINED.

REMBL; RE37322; EATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
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-I- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF FOURTION STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.

-I- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

-I- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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-!- SIMILARIY: BELONGS TO THE BCL-2 FAMILY.
EMBL; L14680; G408947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01080; BCL2.
APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE; MITOCHONDRION.
TRANSMEM 209 230 POTENTIAL.
SEQUENCE 236 AA; 26425 MW; 7ADFE975 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.0%; Score 250; DB 1; Length 236; 30.4%; Pred. No. 1.05e-25; attive 31; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26550 MW; 336E6B40 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BCL2 OR BCL-2 ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94193015.
SATO T., IRIE S., KRAJEWSKI S., REED J.C.;
GENE 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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Best Local Similarity 27.2%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 30.4%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATTUS NORVEGICUS (RAT)
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90 e-vff-rvaadmfsdgnfnwgrvvalfyfasklvlkalctkvpelirtimgwtldf-lre 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 gdragrmggeapelaldpvpgdastkklseclkrigdelds--nmelgrmiaavdtdspr 89
                                                                                 147 rllgwigdgggwdgllsyfgtptwqtvtifvagvltasltiwk 189
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                                                                                                                                                                                                                                                                                                                                                                                 APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
TRANSMEM 172 192 POTENTIAL.
                                       OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
CELL 74:609-619(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 13.2%;
Local Similarity 24.5%;
les 40; Conservative
                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01080; BCL2.
                           MEDLINE; 93364978.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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106 NAYEYFTKIAISLFESGINWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHH 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6 x DBA/2 F1;
MEDLINE; 93364978.
MEDLINE; 93364978.
MEDLINE; 93364978.
CELL 74:609-619(1993).
-!- FOUNCTION ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BCL-2.
-!- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 seqimktgafllqgfiqdragrmagetpeltleqppqdastk-klseclrrigdelds-- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 218; DB 1; Length 192;
Pred. No. 7.08e-20;
50; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAXA_HUMAN STANDARD; PRT; 192 AA.
007812;
01-FEB-1995 (REL. 31, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 AA; 21394 MW; BD035304 CRC32;
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                                                                                                                                                                                                                                                                                                            192
                                                                                                                                                                182 -1htwiqdnggwdafvel-ygpsmrpl 206
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166 CIARWIAQRGGWVAALNLGNGPILNVL 192
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Local Similarity 25.6%;
les 46; Conservative
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                   LT 10
BAXA_MOUSE
Q07813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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ID BP
AC OC
OT OT
DT OT
DT OT
DE AL
GN BL
OC ER
RN C C
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Length 192; 71; Indels

Score 206; DB 1; I Pred. No. 9.65e-18; 45; Mismatches 71;

172 192 POTENTIAL. 192 AA; 21184 MW; B2E6148A CRC32;

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                                                                                                                                                                                                                                                                                -:- SUBCULIT: FORMS HOMOIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
-:- SUBCELLUIAR LOCATION: CYTOPLASMIC.
-:- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
-:- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
PPIR; B47538; B47538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                  OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
CELL 74:609-619(1993).
-!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BCL-2.
                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 201; DB 1; Length 218;
Pred. No. 7.31e-17;
36; Mismatches 58; Indels
                           01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, CYTOFLASMIC ISOFORM BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSTIE; PS01080; BCL2.
APOPIOSIS; ALTERNATIVE SPLICING.
SEQUENCE 218 AA; 24220 MW; 82B2FF09 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 27.0%;
Matches 37; Conservative
 STANDARD;
                                                                                                             HOMO SAPIENS (HUMAN).
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                       MEDLINE; 93364978.
BAXB_HUMAN
Q07814;
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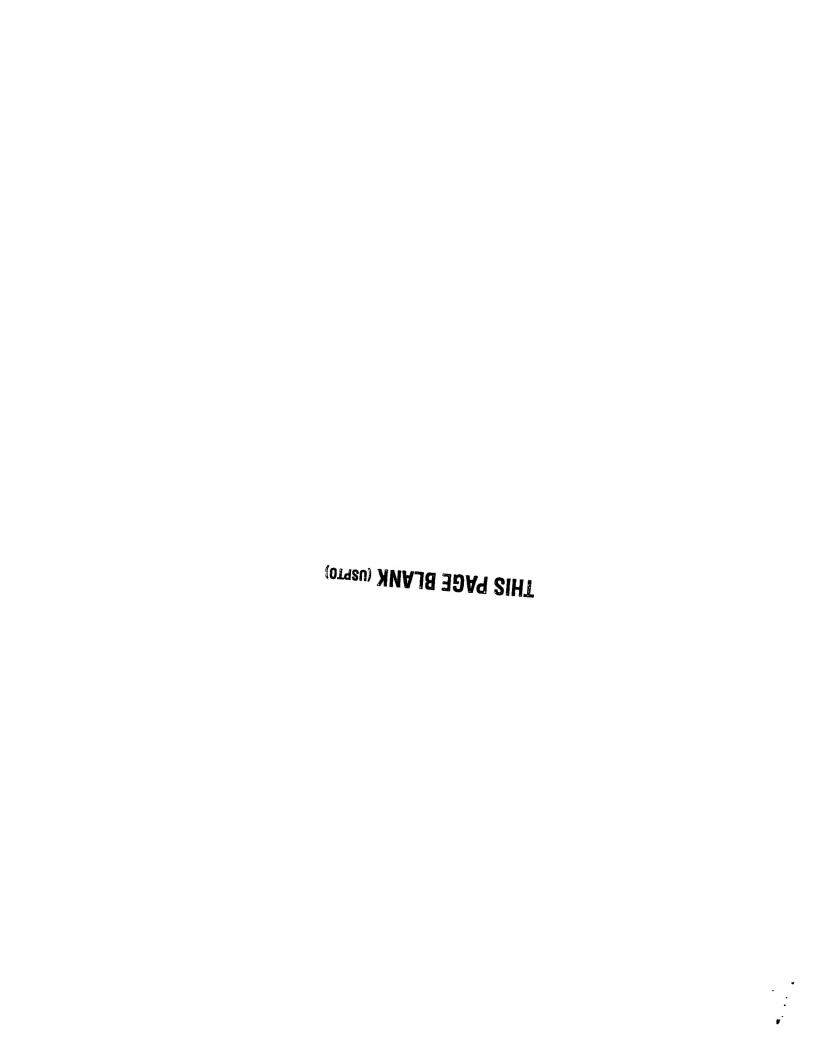
HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.

[1] SEQUENCE FROM N.A.

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EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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-!- INDUCTION: EXPRESSION INCREASES EARLY DURING PHORBOL-ESTER INDUCED DIFFERENTIATION ALONG THE MONOCYTE/MAGROPHAGE PATHWAY IN WYELOID LEUKEWIA CELL LINES ML-1.
-!- SIMILARITY: BELONGS TO THE BCL2 FAMILY.
EMBL; L08246; -; NOT_ANNOTATED_CDS.
MIM; 159552; -,
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                                                                                                                                                                     174 lyrqsleiisrylreqatgakdtkpmgrsgatsrkaletlrrvgdgvqrnhetvfqgmlr 233
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32 gdragrmggeapelaldpvpgdastkklsecikrigdelds--nmelgrmiaavdtdspr 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOZOPAS K.M., YANG T., BUCHAN H.L., ZHOU P., CRAIG R.W.;
PROC., NATL. ACAD. SCI. U.S.A. 90:3316-3520(1993).
-1. FUNCTION: INVOLVED IN PROGRAMMING OF DIFFERENTATION AND
CONCOMITANT MAINTENANCE OF VIABILLITY BUT NOT OF PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAX.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCLI_HUMAN STANDARD; PRT; 350 AA.
007820;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 12.3%; Score 192; DB 6; Length 350; Local Similarity 24.3%; Pred. No. 2.70e-15; nes 34; Conservative 40; Mismatches 63; Indels
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10194B64 CRC32;
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01-0cT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BAX PROTEIN, CYTOPLASMIC ISOFONM DELTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 AA.
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PROSITE: PS01080; BCL2.
APOPTOSIS; TRANSMEMBRANE; DIFFERENTIATION.
227 227 DOTTENTIAL.
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TISSUE-MYELOID LEUKEMIA CELLS;
MEDLINE; 93234528.
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P55269;
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SEQUENCE FROM N.A.
MEDLINE; 95331797.
APTE S.S., MATTEL M.-G., OLSEN B.R.;
GENOMICS 26:592-594(1995).
-I- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE PROLOCORION: CYTOPLASMIC (POTENTIAL).
-I- SUMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIN E.Y., ORLORSKY A., BERGER M.S., PRYSTOWSKY M.B.;
J. IMMUNOL. 151:1979-1988(1993).
-!- FUNCTION: MAY FUNCTION IN THE RESPONSE OF HEMOPOIETIC CELLS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 rivtifafggvllkklpqeqialdvcaykqvssfvaefimnn-tgewirqnggw 140
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                             Match 11.3%; Score 177; DB 1; Length 143; Local Similarity 27.4%; Pred. No. 9.88e-13; es 29; Conservative 31; Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN (A1 PROTEIN)
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163 LHHCIARWIAQRGGWVAALNIGNGPI-LNVLVVVLGVVLLGQFVVRR 207
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APOPTOSIS; ALTERNATIVE SPLICING.
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SEQUENCE 172 AA; 19914 MW; FFD38D6F CRC32;
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STRAIN-CBA/J; TISSUE-BONE MARROW;
MEDLINE; 93346743.
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Matches
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Search completed: Wed Aug 20 11:02:15 1997 Job time : 21 secs.



Release 2. Copyright Di	2.1D John F. Collins, Biocomputing Research Unit. t (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a.	n.a. database search, using Smith-Waterman algorithm
Run on: T Tabular output not	Thu Aug 21 12:30:31 1997; MasPar time 1065.82 Seconds 1326.187 Million cell updates/sec not generated.
	>US-08-320-157-8 (1-1287) from US08320157.seq
N.A. Sequence: Comp:	1 TTTTAATATAATTAATGTGCCTCAAGAGTACAGAAGCTT 1287 AAAATTATATTAATTACACGGAGTTCTCATGTCTTCGAA
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Statistics: M	Mean 11.725; Variance 5.132; scale 2.285

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eucheria; Putheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6478)
Kiefer,M.C., Brauer,M.J., Powers,V.C., Wu,J.J., Umansky,S.R.,
Tomei,L.D. and Barr,P.J.
Modulation of apoptosis by the widely distributed Bcl-2 homologue
              Pred. No. 0.00e+00 0.
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Human DNA sequence fr
Human BAC clone RG062 7
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Trypanosoma brucei MV
C.roseus stri gene.
C.perfingens DNA for D.melanogaster fsh me 7
Soybean phytochrome B 2
Snake (green habu) grTBP g
Snake (green habu) gr
Caenorhabditis elegan
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Kriefer, M.C.
Direct Submission
Submitted (02-NOV-1994) Michael C. Kiefer, Mol. Biol.,
                                      Human Bak-2 gene, com
H.sapiens BAK mRNA fo
Human Bak mRNA, compl
Human Bak-3 pseudogen
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Woodchuck intronless
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Human DNA sequence fr
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T.thermophila G8-scRN
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HS162C6
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Nature 374 (6524), 736-739
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AUTHORS
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/product="Bak-2 protein"
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/dranslation="MaSGGGFPRQECGEPALPSASEEQVAQDTEEVFRSYVFYHHQ
QEOEARGAARAPDEMYTLPLQPSSTMGQVGRQLAITGDDINRRYDSEEQTMLOHLQP
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                                            /clone_lib="pWE 15/Human genomic/chromosome="20"
                                                                                                                                                                                 Score 1269; DB 77;
Pred. No. 0.00e+00;
0; Mismatches 0;
                           /organism="Homo sapiens"
 Location/Qualifiers
1..6478
                                                                         /gene="Bak-2"
                                      /clone="A4"
                                                                                                                                                                                Query Match 98.6%;
Best Local Similarity 99.8%;
Matches 1287; Conservative
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/codon_start=1
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/db_xref="P1D:g804985"
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QEQEAEGVAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQPLQP
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                             catcattggggacgacatcaaccgacgctatgactcagagttccagaccatgttgcagca
                                                                                       tgagagtggcatcaattggggccgtgtggtggttgttcttctgggcttcagctaccgtctggc
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Direct Submission
Submitted (25-JAN-1995) R. Brown, Glaxo Researd
Greenford Road, Greenford, Middlesex UB6 OHE,
Location/Qualifiers
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/tissue_type="B-cell"
/clone_lib="EBV-transformed
193..828
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TAENAXEYFTKIATSLFESGINMGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVD FMLHHCIARWIAQRGGWVAALNLGNGPILNVLVVLGVVLLGOFVVRRFFKS" 405 c 400 g 298 t ä 1011 1131 1071 1191 480 099 720 780 840 180 240 300 360 420 771 540 891 900 531 591 651 711 831 951 411 9 Gaps gacccagagatggtcaccttacctctgcaacctagcagcaccatgggggcaggtgggacgg ttgcagcacctgcagcccacggcagagaatgcctatgagtacttcaccaagattgccacc 5; Length 1360; Indels 15; Score 894; DB 73; Pred. No. 0.00e+00; 0; Mismatches 15; Query Match 69.5%; Best Local Similarity 98.2%; Matches 921; Conservative ಥ 257 BASE COUNT ORIGIN 412 532 592 652 832 952 1012 1132 181 712 892 841 1192 61 121 241 361 421 772 481 541 601 661 781 301 9 9 g õ ద ò ద ò ద ŏ ద 5 8 ö g õ g ò g 5 5 6 ò 8 P ద ò g ò g ò

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Submitted (30-MAR-1995) Thomas Chittenden, Apoptosis Technology
Inc., 148 Sidney St., Cambridge, MA 02139, USA

Location/Qualifiers
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Chittenden, T., Harrington, E.A., O'Connor, R., Flemington, C., Lutz, R.J., Evan, G.I. and Guillad, B.C.
Induction, of apoptosis by the Bcl-2 homologue Bak
Nature 374 (6524), 733-736 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/clone_lib="Jurkat cell cDNA library (Stratagene)"
/cell_line="Jurkat cell"
65..700
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715 CCAGAGATGGTCACCTTACCTCTGCAACCTAGCACCATGGGGCAGGTGGGACGCAG
                                                                                                                   ctgtttgagagtggcatcaattggggccgtgtggtggttcttctgggcttcggctaccgt
                                                                                                                                      895 CTGTTTGAGAGTGGCATCAATTGGGGCCGTGTGGTGGCTCTTCTGGGCTTCAGCTACCGT
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Human Bak protein mRNA, complete cds.
U23765
9758797
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Chittenden, T.
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     FMLHHCIARWIAQRGGWVAALNLGNGPILNVLVVLGVVLLGQFVVRRFFKS"
1949
                                                                                     Gaps
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                                                           Score 768; DB 77; Length 19
Pred. No. 0.00e+00;
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Richmond, CA 94804, USA
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eubheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 5408)
Kiefer, M.C., Brauer, M.J., Powers, V.C., Wu, J.J., Umansky, S.R.,
Tomei, L.D. and Barr, P.J.
Modulation of apoptosis by the widely distributed Bcl-2 homologue
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y South, P
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/clone_lib="pWE 15/Human genomic
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Direct Submission
Submitted (02-NOV-1994) Michael C. Kiefer,M.C.
Biotechnology Inc., 1401 Marina Way & Location/Qualifiers
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IMPORTANT: This sequence is unfinished and does not necessarily
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Human DNA sequence *** SEQUENCING IN PROGRESS
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       Pred. No. 1.52e-129;
0; Mismatches 8;
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ACCESSION 128278
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Ablaret-pid:g1655494"

/translation-"MLCHLOPTAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLA
LHYYQHGLTGFLGQVTRFVVDFMLHHCIARWIAQRGGWVAALNGNGPILNVLVVLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and Bak, as well as susceptibility to therapeutic agents of human breast cancer cells Unpublished (1996)

Location/Qualifiers
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Human DNA for apotosis-regulator Bak, exon 2, 3 and partial cds
D88397
                                                                                                                                      306 GCTGGCACCTC-ATGATCACTGGAGTCTCGCGGGTCCCTCAGGCTGCACAGGGACAAGTA 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hidetaka Buchi, Saitama Cancer Center Research Institute, Depertment of Biochemistry; 818 Komuro, Ina, Kita-adachi-gun, Saitama 362, Japan (E-mail:hide@saitama-cc.go.jp, Tel:048-722-111(ex.255), Fax:048-722-1739)
Eguchi, H. and Hayashi, S.
/clone="291J10"
/chromosome="6"
Sequence 123579 BP; 28765 A; 27932 C; 27951 G; 27528 T; 11403 other;
                                                                                             Gaps
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
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                                                                                           2; Indels 1;
                                                            Length 123579;
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                                                            Score 198; DB 5; L
Pred. No. 3.97e-149;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                   Db 108032 caccogggttgggccaggatcccggcagg 108060
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2 of 2
                                                            Query Match
Best Local Similarity 98.6%;
Matches 206; Conservative
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Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and Bak, as well as susceptibility to therapeutic agents of human breast cancer cells
Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-0CT-1996) to the DDBJ/EMBL/GenBank databases. Hidetaka Eguchi, Saitama Cancer Center Research Institute, Depertment of Biochemistry; 818 Komuro, Ina, Kita-adachi-gun, Saitama 362, Japan (E-mail:hide@saitama-cc.go.jp, Tel:048-722-1111(ex.255), Fax:048-722-1739)
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal diseasal
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use (control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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                                                                                                                                                                                               57; Length 215;
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71; Mismatches 69; Indels
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Pred. No. 1.16e-06;
85; Mismatches 96; Indels
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Best Local Similarity 11.2%;
Matches 23; Conservative
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Best Local Similarity 16.0%;
Matches 27; Conservative
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PECAM-1 (CD31) cloning and relation to adhesion molecules of thimmunoglobulin gene superfamily
Science 247 (4947), 1219-1222 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heat shock induced; RNA polymerase III; scRNA.
Tetrahymena thermophila.
Tetrahymena thermophila
Eukaryotae; mitochondrial eukaryotes; Alveolata; Ciliophora;
Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
Hallberg, R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA polymerase
HUMPECAM16 250 bp DNA PRI 07-JAN-1995 Homo sapiens platelet/endothelial cell adhesion molecule-1 (PECAM-1) gene, partial intron 13.
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Kirschbaum, N.E., Gumina, R.J. and Newman, P.J.
Organization of the gene for human platelet/endothelial cell
adhesion molecule-1 shows alternatively spliced isoforms and
                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
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Submitted (18-DEC-1990) R.L. Hallberg, SYRACUSE UNIVERSITY,
DEPARTMENT, 130 COLLEGE PLACE, SYRACUSE NY 13244, USA
2 (bases 1 to 1049).
Hallberg, E.M., Fung, P. and Hallberg, R.L.
Genomic sequence encoding a heat shock-induced, RNA polymera
III-transcribed RNA from Tetrahymena thermophila
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Pred. No. 1.44e-01;
0; Mismatches 27; Indels
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platelet endothelial cell adhesion molecule
16 of 27
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Blood 84, 4028-4037 (1994)
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/organism="Homo sapiens"
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<1..>250
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X57037
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/citation=[2]
/number=13
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QKFDLMYAKRAFVHWYVGEGMEEGEFSBAREDLAALEKDYEEVGIESNBAEGEDEGYE
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X.Laevis POMC-A gene for proopiomelanocortin-A.
X59370 S35811
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/organism="Xenopus laevis"
/clone_lib="lambda EMBL4"
/clone="lambda XPA5"
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462..469
491..538
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Local Similarity 67.3%;
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Xenopus laevis
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Submitted (27-JUL-1989) Hyde J.E., University of Manchester Institute of Science and Technology, Dept of Biochemistry and Applied Molecular Biology, UMIST P O Box 88, Manchester M60 LQD, UK 2 (bases 1 to 2648)
HOLDOWRY,S.P., S.Ims. P.F., Delves,C.J., Scaife,J.G. and Hyde,J.E. Isolation of alpha-tubulin genes from the human malaria parasite, Plasmodium falciparum: sequence analysis of alpha-tubulin Microbiol. 3 (11), 1501-1510 (1989)
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NDDAFNTFFSETGAGKHVPRCVFVDLEPTVVDEVRTGTYRQLFHPEQLISGKEDAANN
FARGHYTICKEWIDVCLDRIRKLADMOTGLOGFLMYSAVGGTGSGFGCLMLERLSVD
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IERPPYTNLMRLIADVYSTRAPSCALMYDVTEFGTNLVPYPRHHEMLSSYAPVY
SAEKAXHEQLSVSEITNSAFEPANMMAKCDPRHGKYMACCLMYRGDVVPKDVNAAVAT
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malaria parasite.
Plasmodium falciparum
Eukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa;
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Pred. No. 1.44e-01;
0; Mismatches 23; Indels 1;
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                                                                         /organism="Tetrahymena thermophila"
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/cell_type="intraerythrocytic"
/clone_lib="lambda NM1149, HindIII"
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424..432
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/db_xref="SWISS-PROT:P14642"
20 (4), 912 (1992)
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Deen, P.M., Roubos, E.W. and Martens, G.J.
Presence of Vi-transposon-like elements in the proopiomelanocortin gene A of Xenopus laevis does not affect gene activity
Mol. Gen. Genet. 230 (3), 491-493 (1991) .; 7 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus. 1 (bases 1 to 9747) Deen,P.M.T. Comparative structural analysis of the transcriptionally active proopiomelanocortin genes A and B of Xenopus laevis Mol. Biol. Evol. 9 (3), 483-494 (1992) neuropeptide/opioid; opioid (beta-endorphin); POMC-A gene; preprohormone; proopiomelanocortin-A; repetitive element JH12; repetitive element Vi; secretion. Gaps 02-DEC-1993 colour adaptation; corticotrope (ATCH); melanotrope (a-MSH); Submitted (03-MAY-1991) P.M.T. Deen, Univ of Nijmegen, Toernnoolveld, 6525 ED Nijmegen, THE NETHERLANDS 2 (Dases I to 9747)
Deen, P.M.T., Terwel, D., Bussemakers, M.J.M., Roubos, E.W. and Martens, G.J.M.
Comparative analysis of the transcriptionally active Propolomelanocortin genes A and B of Xenopus laevis 4 (bases 1 to 9747) Deen, P.M., Bussemakers, M.J., Terwel, D., Roubos, E.W. and Martens, G.J. .; ;

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;

Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;

Tracheata; Hexapoda; Insecta; Pterygota; Strepsiptera; Stylopoidea;

Stylopidae; Xeninae; Xenos.

1 (bases 1 to 610)

Whiting, M.F., Carpenter, J.C., Wheeler, Q.D. and Wheeler, W.C.

The Strepsiptera Problem: Phylogeny of the Holometabolous Insect
Orders Inferred From 188 and 288 Ribosomal DNA Sequences and
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Whiting,M.F., Carpenter,J.C., Wheeler,Q.D. and Wheeler,W.C.
Direct Submission
Submitted (25-JUL-1996) Entomology, American Museum of Natural
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Pred. No. 1.44e-01;
0; Mismatches 16; Indels 1;
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Xenos pecki 28S ribosomal RNA gene, partial sequence.
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91762761
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6886..7347
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######################################	Nmatch STD : Dbase 0; Query 0	134151 segs, 4	Post-processing: Minimum Match 0% Listing first 45 summaries	Database: n-geneseq27 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27	Statistics: Mean 9.436; Variance 5.783; scale 1.632	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID Description Pred. No.	1 1280 99.5 1286 24 T42139 Bak-2 gene. 0.00e+00 3 890 69.2 2094 24 T42139 Bak gene. 0.00e+00 0.00e+00 4 889 69.1 2072 14 095492 Burman Cdn-1 cDnA. 0.00e+00 0.00e+00 5 768 59.7 1968 19 T17375 Burman Cdn-1 cDnA. 0.00e+00

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HCV envelope region 1.74e-03
Generic DNA sequence 1.73e-02
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latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents Sequence 1286 BP; 298 A; 341 C; 328 G; 319 T;
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                                                              Length 1286;
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                                                           Score 1280; DB 24;
Pred. No. 0.00e+00;
0; Mismatches 0;
                                                           99.5%;
Local Similarity 99.9%;
nes 1286; Conservative
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gacttcatgctgcatcactgcattgcccggtggattgcacagaggggtggctgggtggca
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Claim 6, Fig. 5A-H; 66pp; English.

Claim 6, Fig. 5A-H; 66pp; English.

Can-2 cDNA was isolated from a human placental genomic library using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (R77876).

Sequence 6511 BP; 1513 A; 1620 C; 1605 G; 1773 T;
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Pred. No. 0.00e+00;
0; Mismatches 0; Indels
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30-NOV-1994; U2-160067.
07-OCT-1994; US-160067.
(LXRB-) LXR BIOTECHOLOGY INC.
BAIR PJ. Klefer MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.8%;
Matches 1287; Conservative
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Q95493 standard; DNA; 6511
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21-NOV-1995 (fi.
Human Cdn-2 DNA.
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WO9515084-A.
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Score 890;
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                              T
T42138 standard; cDNA; 2094
                                                                                                                                                                                                                                                                                                                                                          Query Match 69.2%;
Best Local Similarity 98.2%;
Matches 917; Conservative
                                           T42138;
22-FEB-1997 (first entry)
                                                                                                                                                                                    20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY
Barr PJ, Kiefer MC;
WPI; 96-485886/48.
                                                                                                                            201..836
                                                                                                                                           protein
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19-APR-1996; U05639.
20-APR-1995; US-4265
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/product= Bak p
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                                                                 cccactcagccctgggagcagccgccagccctcgggacctccatctccacctgc
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Disclosure; Fig 1; 24pp; English.

The sequence encodes Bak protein, which is a bcl-1 homologue which
The sequence encodes Bak protein, which is a bcl-1 homologue which
The sequence encodes Bak protein, which is all live carly lytic cycle BHREI
The protein, and is capable of modulating apoptosis. The Bak gene is
Located on human chromosome 6 at 6p21-23. The protein may be used
in complete or partial form, or as an epitope tag fusion protein,
In a new virucide drug screening method, which involves combination
of Bak protein and a viral protein (e.g. EBV BHREI), exposure to a
test compound, and monitoring for disruption of the interaction,
Ce.g. by co-precipitation, protein interactive trapping or ELISA.
Interaction of Bak and viral proteins allows viral replication or
Interaction may be used as virucide, antitumour or diagnostic agents.
Sequence 2094 BP; 410 A; 608 C; 606 G; 470 I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311
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Human; Bak; apoptosis; latency; virus replication;
Spetein-Barr virus; BHRR1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic; ss.
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Now nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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Cdn-1 CDNA was isolated from a human heart cDNA library using a proviously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HT29 cells. Expression of
                      ccagagatggtcaccttacctctgcaacctagcagcaccatggggcaggtgggacggcagflillillillillillillillillillillccagacagcag
                                                                                   9t9gtcgacttcatgctgcatcactgcattgcccggtggattgcacagaggggtggctgg
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Homo sapiens.
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188..903
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30-NOV-1994, U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LX BIOTECHNOLOGY INC.
BAXT PJ, KIEÉE MC;
WPI; 95-215106/28.
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095492 standard; cDNA; 2072
095492;
21-NOV-1995 (first entry)
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WI-L2 lymphoblastoid cells resulted in inci
in response to anti-Fas-mediated apoptosis
2072 BP; 404 A; 603 C; 598 G;
                                                            Score 889; DB 14;
Pred. No. 0.00e+00;
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                                                              th 69.1%;
| Similarity 98.2%;
916; Conservative
                                                                            Best Local Similarity
                                  Sequence
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shock; lymphoma; eczema; ss.
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Local Similarity 91.0%;
les 886; Conservative
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Q95494 standard; DNA; 5408
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Human Cdn-3 DNA.
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WPI; 95-215106/28.
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Claim 6; Fig 4; 100pp; English.

A full-length cDNA clone (T17375) codes for Bcl-Y (R81451), a protein that induces apoptosis in cells and functions as a negative regulator of Bcl-2 function. It was isolated from a Jurkat cell cDNA library using as probe a partial Bcl-Y cDNA clone obtd. by PCR of DNA derived from the Namalwa cell line. The cDNA can be used for prodn. of recombinant Bcl-Y, as a probe, to produce transgenic animal models, and in the gene therapy of disorders characterised by inappropriate cell proliferation or cell death.

Sequence 1968 BP; 382 A; 560 C; 576 G; 450 T;
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W0960232-A1.

22-FBE-1996, U10103.

09-AUG-1994; US-287427.

11-OCT-1994; US-221071.

Chittenden TD;

WPI; 96-139648/14.

P-PSDB; R81451.

P-PSDB; R81451.

Wew isolated human BCl-Y protein - used to develop prods. for treating disorders characterised by inappropriate cell proliferation or cell death
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                                               cell death; diagnosis;
                                             Bcl-Y; apoptosis; cell proliferation;
gene therapy; ss.
                                                                          Location/Qualifiers
65..700
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          standard; cDNA; 1968
                          02-JUL-1996 (first entry)
Bcl-r cDNA.
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Southern blot analysis of human genomic DNA and a panel of human, rodent somatic cell DNAs revealed at least 3 Cdn-related genes residing on chromosomes 6, 11 and 20. Cdn-3 (R77878) did not contain the structural features of Cdn-1 (R77876), Cdn-2 (R77877) or other Bcl-2 family members.
Sequence 5408 Bp; 1369 A; 1384 C; 1314 G; 1341 T;
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Pred. No. 0.00e+00;
0; Mismatches 79; Indels
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-CCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
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                 1797 aggaacaggaggctgaagggggggggcgccctgccgaccagagatggtcaccttgcccc 1856
                                                                                                                              1857 tecaacetageageaceatggggcaggtgggaeggeagetegeeateaceagg-aegaea 1915
                                                                                                                                                                   1916 tcaaccggcactatgacttcggagttccagaccatgctgcagcacctgcagcccacggca 1975
                                                                                                                                                                                                      1976 gagaacgeetacgagtaetteaceaagategeeteeageetgtttgagagtggeateaae 2035
                                                                                                                                                                                                                                                                                2096 cacggettgactggettectgggeetggtgaceegettegtggt---etteatgetgeaa 2152
                                                                                                                                                                                                                                                                                                                     2153 caaggeategeeeggtggatetegeagagggeggetgggtggeageeetggaettggge 2212
                                                                                                                                                                                                                                                                                                                                       1036 CACTGCATTGCCCGGTGGATTGCACAGAGGGGTGGCTGGGTGGCAGCCCTGAACTTGGGC 1095
                                                                                                                                                                                                                                                                                                                                                                          1096 AATGGTCCCATCCTGAACGTGCTGGTTCTGGGTGTGGTTCTGTTGGGCCCAGTTTGTG 1155
                                                                                                                                                                                                                                                                                                                                                                                             1215 CCTGCCTGGACTTAAGCGAAGTCTTTGCCTTCTCTGCTCC-TTGCAGGG-TCCCCCCTCA 1272
                                                                                                     915
497 GCCAGGATCCCGGCAGGCTGATCCCGTCCTCCACTGAGACCTGAAAAATGGCTTCGGGGC 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Natriuretic Peptide Receptor B. NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase; hyperaldosteronism; glaucoma; guanyl cyclase.
                                                                                                                                                                                                                   2036 cggggccgtgtggtggctctcctgggcttcggctaccgtctggtcctacatgtctaccag
                                                                                                                                                                                                                                                        916 TGGGCCGTGTGGTGGTCTTTCTGGCTTCAGCTACCGTCTGGCCCTACACATCTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                 2333 cctgcctggacttaagccaagtctttgccttccccactcccttgcaggggtcaccttca
                                                                                                                                                                                                                                                                                                   976 CGTGGCCTGACTGGCTTCCTGGGCCAGGTGACCCGCTTTGTGGTGGACTTCATGCTGCAT
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/label- extracellular domain

/note- "binds natriuretic peptides A,B and C]"

/notel- 456..456

/label- transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q10572 standard; DNA; 1047 BP
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09-APR-1991 (first entry)
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/label- signal sequence
Protein 12
/label- mature NPBR
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1287 AAGCTTCTGTACTCTTGAGGGGGGGCCTCCTGCAAGGAGGCAGAGAGGCAAAGACTTCGCTT 1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1109 AGGATGGGACCATTGCCCAAGTTCAGGGCTGCCACCCAGCCACCCCTCTGTGCAATCCAC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 rknmnnknnasmnwrnrwnnnngnsnryhkgagsrntnsnrgssygsnmtahgkynnna 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 ndgnrnvnkmngrryhgvtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknn 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natilureic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B. NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the produ. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of matriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 G;
                       /note= "GC and protien kinase activity"
Modified -site 24..26
/label= N-glycos_site
Modified -site 35..37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang M, Goeddel D, Lowe D;
WPI; 91-036711/05.
N-PSDB; Q10324.
'label= cytoplasmic domain
                                                                                                                                                                                                                                                                                                             /label= N-glycos_site
Modified -site 277..270
/label= N-gros_site
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/label- N-glycos_site
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Modified -site 349..351
/label= N-glycos_site
Modified -site 600..602
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23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M, Goeddel D, LOW
                                                                                                                                                 /label= N-glycos_site
Modified -site 161..1
/label= N-glycos_site
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Modified -site 244..2
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Location/Qualifiers 19..69
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 nrsgnnynngndnsnknnvnkvrngnrnynrnsndrtnnnnnnnnnnrcwandnanrnd 778
                                                                                                                     899 nndvykvntngdaymvvsgnngrngnrhannnarmananndavssnrnrhrnh-dnnrnr 957
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Human Natriuretic Peptide Receptor B.
NPRBi, ANP: BNP; CNP; kidney failure; heart failure; protein kinase;
hyperaldosteronism; glaucoma; guanyl cyclase.
                                                         CATAGCGTCGGTT-GATGTCGTCCCCAATGATGGCGAGCTGCCGTCCCACCTGCCCCATG
                                                                                                                                  ngnnkgnnrrnnknggtsnndnnnrmnnyannnnknvnnrtnaynnnkrkanannynnn
                                                                                                 GTGCTGCTAGGTTGCAGGGTAAGGTGACCATCTCTGGGTCGGCAGGGGCAGCCGCCCCT
                   870 CTCATAGGCATTCTCTGCCGTGGGCTGCAGGTGCTG-CAACATGGTCTGGAACTCTGAGT
                                                                              nhsvannnkrgntvnanandsvtnynsdnvgntansanstnmnvvtnnndnytcndannd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natilurelic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "GC and protten Kinase activity"
Modified -site 24..26
/label= N-glycos_site
Modified -site 35..37
/label= N-glycos_site
                                                                                                                                                                                                                                                                                                                                                                                                             'note= "binds natriuretic peptides A,B
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Q10572 standard; DNA; 1047 BP
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extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                   'label - transmembrane domain
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22-JUN-1990; U03586.
23-JUN-1989; US-370673.
(GETH ) GENENTECH IUC.
Chang M, Goeddel D, Lowe D;
WPI; 91-036711/05.
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Modified -site 244..246
/label N-glycos_site
Modified -site 277..279
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/label* N-glycos_site
Modified -site 195..197
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Protein 12
                                                                                                                                                                                                    1018 nnrgdvnmkgkg 1029
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WO9100292-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 TTTTGGTGTATGAACTGTAGTCCTAGAGGATTTTATTAGTTATGAGTTCTATAACTAAGA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having quanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the produ. Of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              530 ahgkynnnantghnkgnvvankhvnkkrnnntrnvnnnnkhmrdvnnnhntrnngacndn
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                                                                                                                                                                                                                                                                                                                                                            Length 1047;
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 9.3%; Pred. No. 5.42e-31;
Matches 63; Conservative 199; Mismatches 412; Indels
                                                                                                                                                                                                                                                                                               51 T;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1228 TAAGTCCAGGCAGGGTCTGAACTGGGACCCCAAAGGCACCCTTGGGAGTCATGATTTGA 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynv 145
                                                                                                                                                                                                                                                                                          Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                 Random point mutations were introduced into the alpha fragment of Erodia beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonuclectide probe MKI4-A consists of nuclectides 5-95 of MKI4 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 Others;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                            OSTAKK-LJUN, V. (SISO) SUOMEN SOKERI OY. (SISO) SUOMEN SOKERI OY. Tahtovaara P., Knowles J., Koivula A., Bamford J., Reinikainen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 1; Length 204;
Pred. No. 1.24e-11;
57; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1168 AGAATCTTCGTACCACAACTGGCCCAACAGAACCACACGAGAACC 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 9; Length 91;
Pred. No. 1.70e-10;
45; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 hnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvchcc 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 C;
                        /function-multiple cloning site
primer_bind 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 10
Q51746 standard; cDNA; 91 BP.
Q51746;
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01-DEC-1993.
24-MAY-1993. 108325.
25-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
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Best Local Similarity 10.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 A;
                                                                                                                                                         30-MAR-1988; 105163.
03-APR-1987; US-034819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shank DD, Spears PA; WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also P80575.
Sequence 204 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity

Mes 12; Conser
                                                                                                        EP-285123-A.
                                                                                                                                05-MAY-1988.
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Gaps

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3 ctccggcgssvhsyyvvhvvshhhsvhhvvhhvvhvvhhvhhvhyhvyvsvc 61

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Introducing random point mutations into nucleic acods -

Introducing random point mutations into nucleic acods -

The preparation of suppletion of molecules and screening.

The standom point mutations were introduced into the alpha fragment of

E. Coll beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oliqonucleotide was hybridised to

It to generate a popn of DNA molecules which terminate at all

C. possible nucleotide positions within a specified region. The

C. variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the

C. transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable took-vector system

The sequence covers all 176 difft base substitutions, most of which
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NoV-1990 (first entry)
Base substituted E.coli beta galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonuclectide probe MK14-A consists of nucleotides 5-95 of 1(051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1204 GGGACCCCAAAGGCACCCTTGGGAGTCATGATTTGAAGAATCTTCGTACC 1155
                                                                                                                                             31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.3%; Score 42; DB 9; Length 91; 0.0%; Pred. No. 6.22e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function-multiple cloning site
                                                                                                                                                                                                                                                                        01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N81164 standard; DNA; 204 BP
                                                                                     T 11
Q51746 standard; cDNA; 91
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30-MAR-1988; 105163.
03-APR-1987; US-034819.
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WPI; 93-378844/48.
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                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                  281 AACATCATITAAAAAACATTTTTGGCTGGCACCTCATGATCACTGGAGTCTCGCGGGTC 340
                                                                                                                                   95 rrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncc 154
                                                                                                                                                                                                                                                                                                                                                         Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                     Gaps
                                    108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designe allowing direct and rapid detection in a screening process. Sequence 114 Bp. 0 A; 2 C; 2 G; 2 T;
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                                                                  Length 204;
                                                                                                     34; Indels
                                    11 T;
                                                                                                                                                                                                    155 cbnnhvchnvhbnnhrnwayvrhdarrddvhccvchccgat 195
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Pred. No. 1.26e-06;
34; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uence represents '2'; Z can be or 12 nucleotides (see
                                                                                    8.16e-09
                                                                    DB 1;
                                                                                                     53; Mismatches
                                   17 G;
occurred singularly in any given mutant. See also P80575. Sequence 204 BP; 21 A; 47 C; 17
                                                                    Score 40;
                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 55..60
                                                                                                                                                                                                                                                                                                      070468 standard; DNA; 114 BP.
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                                                                                  12.9%;
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                     Conservative
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US-176500.
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/note= "this sequence
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01-FEB-1994; U00977
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Best Local Similarity
Matches 4; Conser
                                                                                  Best Local Similarity
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30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                       05-APR-1995
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screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; page 35, 255pp; English.

070466 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generate formula can also be represented as follows:X(NNB)1(TGC)(NNB)10(TGC)2(NNB)4Z(NNB)8(TGC)(NNB)9.

9Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in 070466-68. Other specified secretated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compons. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908 GCATCAATTGGGGCCGTGTGGTGGCTCTTCTGGGCTTCAGCTACCGTCTGGCCCTACACA 967
                                                                    909 CATCAATTGGGGCCGTGTGGTGGCTCTTCTGGGCTTCAGCTACCGTCTGGCCCTACACAT 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generic DNA sequence to generate a random TSAR-9 petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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bnabanbanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbanbannan 62
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                                                                                                                                                                                                         969 CTACCAGCGTGGCCTGACTGGCTTCCTGGGCCAGGTGACCCGCTTTGTGGTG 1020
                                                                                                                                     63 bnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying proteins or peptide(s) which bind a ligand - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 nbanbanbanbanbanbanbtgcanbanbanbanbanbanbanbanb 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents 'Z'; Z can be a 5, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 12;
Pred. No. 1.26e-06;
31; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection in a screening |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                              JT 14
Q70466 standard; DNA; 114
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Best Local Similarity
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01-FEB-1993;
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31-JAN-1994;
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Gaps

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74; Indels

Similarity 3.6%; 4; Conservative

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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins PT Identifying proteins or behinding domain and an effector domain proteins page 35; 255pp; English.

Disclosure; Page 35; 255pp; English.

Disclosure, Page 35; 255pp; English.

CC 70467 is a generic DNA sequence used to generate random TSAR (Totally Stribetic Affiliaty Readents) peptides. This generate formula can also be crepresented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)17. X and Y are flanking restriction sites (X is not the same as Y) that are constructed by these generic sequences are shown in CK65151-54. TSARS are concatenated by these generic sequences are shown in CK65151-54. TSARS are concatenated by these generic sequences are shown in CK65151-54. TSARS are concatenated by these generic sequences are shown in CK65151-54. TSARS are concatenated by these generic sequences are shown in CK65151-54. TSARS are concatenated by these generic sequences are shown in CK65151-54. TSARS are concatenated by these generic sequences are shown in CK65151-54. TSARS are concatenated as binding domain with a affinity for a ligand and a second effector peptide portion that is chart the expressed peptide contains. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cystesine residues positioned in, or flanking, the unpredicted or variant residues. These residues comprise, peptide, toxin or enzyme, to the specific target or on the concatenated and also replace the function of macromolecules, eg.

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Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affility reagent; synthetic; binding domain;
effector domain; concatemented heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
968 TCTACCAGCGTGGCCTGACTGGCTTCCTGGGCCAGGTGACCCGCTTTGTG 1017
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                                                                                                                                                                                                                                                                                                                                                  /*tag= a //rtag= a //note= this sequence represents 'Z'; Z can be sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                 Location/Qualiflers 55..60
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKGB DM, KRY BK;
WPI; 94-27939/34.
P-PSDB, R65153.
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Q70467 standard; DNA; 114 BP
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933 TCTTCTGGGCTTCAGCTACGGCCCTACACATCTACGAGCGTGGCCTGGCTT 992

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Search completed: Thu Aug 21 13:23:47 1997 Job time : 416 secs.

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......CCTCAAGAGTACAGAAGCTT 1287
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1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST6

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27:EST37 44:EST34 35:EST35 36:EST36 37:EST37 38:EST38

39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44

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57:EST55 58:EST55 56:EST55 56:EST56 67:EST56 67:EST56 67:EST56

57:EST57 58:EST58 59:EST59 60:EST66 67:EST66 67:EST66 67:EST66 69:EST68 69:EST68 66:EST68 66:EST68 67:EST67 77:EST77 78:EST73 74:EST74 78:EST78 79:EST73 74:EST74 78:EST78 78:EST78 74:EST78 78:EST78 78:E
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26:EST20
38:EST32
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50:EST50
56:EST50
68:EST62
68:EST62
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                                       U.K.
Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, Distribution rights by IntelliGenetics, Inc.
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(1-1287) from US08320157.seq
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AAAATTATATTTAATTACAC.
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120:EST120
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140:EST140
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118:EST118 119:EST119 2 123:EST124 124:EST124 2 123:EST128 124:EST124 2 133:EST128 134:EST139 2 133:EST138 134:EST139 2 143:EST138 144:EST149 148:EST148 144:EST149

153:EST153 154:EST154 7 158:EST158 159:EST159 8 163:EST163 164:EST164 9 168:EST168 169:EST164 1 173:EST173 174:EST174

162:EST162 1 167:EST167 1 172:EST172 1 152:EST152 157:EST157

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mRNA BST 02-AUG-1996 embryo NbME13.5 14.5 Mus musculus cDNA to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
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   179:EST179
184:EST184
189:EST189
194:EST194
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mj09a09.rl Soares mou
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AA001756
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AA02014
AA049828
AA050569
WB2028
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AA139013
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H31840
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HUM229F11B
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AA138853
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T54824
AA173916
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AA03957
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180:EST180
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accacgcggccccagctgatgccactcttaaataggctggaggcgatcttggtgaagagt 381
                                                                                                                      382 tegtaggeatteceggetgtgggetgaagetgttetagtaaattetggaaetetgtgteg 441
                  coggicaaaccacgciggiagacgiacagggccagacggiagccaaagcccaggagaggcc 321
                                869 TCATAGGCATTCTCTGCCGTGGGCTGCAGGTGCTGCAACATGGTCTGGAACTCTGAGTCA
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1 (bases 1 to 497)

Marta,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
Washlogton University School of MedicineP
Washlogton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI: 265450
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Pred. No. 0.00e+00;
0; Mismatches 101; Indels
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                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 272; DB 85; Length 30 Pred. No. 0.00e+00; 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                           1.303
/organism="Homo sapiens"
/clone="231262"
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The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                        90
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Best Local Similarity 95.7%;
Matches 291; Conservative
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19.7%;
78.5%;
                                                                            Conservative
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                                                               Similarity 384; Conser
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Bacsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoch,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                            545 bp mRNA EST 11-SEP-1996
Soares mouse p3NMF19.5 Mus musculus cDNA clone 329622
SW:BCLX_HOMAN Q07817 APOPTOSIS REGULATOR BCL-X.;
                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                          672
                                                cctctgcaacctagcagcaccatggggcaggtgggacggcagctcgccatcattggggac 239
                                                                                                                                                  733 CCTCTGCAACCTAGCAGCACCATGGGGCAGGTGGGACGGCAGCTCGCCATCATTGGGGAC 792
63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:211022
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washu-HHMI Mouse EST Project
Washington University School of MedicineP
Text: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
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mb16g04.rl s
similar to s
W42014
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AUTHORS
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 61
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KEYWORDS
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AA049970 446 bp mRNA EST 09-SEP-1996 mj39b01.rl Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA clone 478441 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                           1109 AGGATGGGACCATTGCCCAAGTTCAGGGCTGCCACCCAGCCACCCCTCTGTGCAATCCAC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                              149 aggatggggactctacgaaaattcagggctgccacccaaccgcctctgtgcgatccat 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctggcgatgtaatgatgcagtatgatatcagccaaaaagcaggtcacctggcccaggaag 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           accacgcggccccagctgatgccactcttaaataggctggaggcgatcttggtgaagagt 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        929 ACCACACGCCCCAATTGATGCCACTCTCAAACAGGCTGGAGGCAATCTTGGTGAAGTAC 870
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                      S)
                                                                                                                      Length 545;
                                                    others
                                                                                                                                                                   Indels
/lab_host="DH10B (ampicillin resistant)"
<1...>545
1 139 c 165 g 105 t 2 other
                                                                                                                                                                      Mismatches 100;
                                                                                                                      Score 254; DB 153;
Pred. No. 0.00e+00;
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source

FEATURES

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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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WashD-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Soares mouse embryo NbME13.5 14.5"
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Min. 286320
Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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88
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                                                         Mus musculus
                                  house mouse
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                                                                                                                                                                                                                                                                      /notes-Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I: oligo(dr) primer [5] strand cDNA regrand. To the was primed with a Not I: oligo(dr) primer [5] regrand. To the with a Not I: oligo (dr) primer [7] regrand. To the with a Not I: oligo (dr) primer [7] regrand. To the with a nounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed by Bento Soares and W.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 314 286 1810
Email: mousgest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:289185
Possible reversed clone: similarity on wrong strand
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1180 GTCATGATTTGAAGAATCTTCGTACCACAAACTGGCCCAACAGAACCACCACCAGAACCA 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mj09a09.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus CDNA AA049828 91529499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           940 CCAGAAGAGCCACACGGCCCCAATTGATGCCACTCTCAAACAGGCTGGAGGCAATCT 881
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Pred. No. 0.00e+00;
0; Mismatches 72; Indels
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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t
                                                                                                                                                                                                                               /organism-"Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="unknown'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.9%;
Matches 304; Conservative
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heart, Lambda ZAP Express vector-Lambda ZAP Express host-E. Coll XL1-Blue Rsitel-EcoRI Rsite2-XhoI mRNA was purified from human fetal hearts (8-10 weeks). CDNA was synthesized using a XhoI-Oligo digastion with XhoI, for directional cloning into predigested lambda ZAP Express.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
   {\tt KK4271F} Homo sapiens cDNA clone {\tt KK4271} 5' similar to BAK FOR BCL-2 HOWOLOGUE.
                                                                                                                                                                                                                                 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopteryqil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
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mouse p3NMF19.5 Mus musculus cDNA clone 403896
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human clone=KK4271 primer=GAAATTAACCCTCACTAAAGGG library=Fetal
                                                                                                                                                                                                                                                                                                                                                                                                           Molecular Cardiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Fal: 4169788758
Fax: 4169785650
Email: liewcc@utcc.utoronto.ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 232;
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Pred. No. 3.44e-64;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="KK4271"
<1..>232
                                                                                                                                                                                                                                                                                                                                       cDNAs from fetal heart
Unpublished (1996)
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Best Local Similarity 96.9%;
Matches 62; Conservative
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mf02e01.rl Soares
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g1393105
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Marra,M., Hillter,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                  Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 ctttcgaagctacgttttttacctccaccagcaggaacaggagacccagggg 361
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Pred. No. 4.27e-87;
0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
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Best Local Similarity 79.7%;
Matches 137; Conservative
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AA050569
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source

FEATURES

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rat primer=M13 Reverse library=Rat PC-12 cells, untreated vector=pBluescript SK- Rsitel=EcoRI Rsite2=XhoI poly(A)+ RNA was purified from untreated PC12 cells cultured for 9 days. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda 2AP II Vector Kit by Stratagene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.

1 (Jases 1 to 279)
Lee, N. H., Weinstock, K. G., Kirkness, E. F., Earle-Hughes, J. A., Fuldner, R. A., Marmaras, S., Glodek, A., Gocayne, J. D., Adams, M. D., Comparative expressed sequence tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment
                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301869905b
Fax: 3018699423
Email: nhlee@tigr.org
For clone availability please contact the TIGR Database (tdbinfo@tdb.tigr.org).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 cogtoccottotgaacagoaggttgcccaggacacagagaggtctttcgaagctac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 320;
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Other_ESTs: EST106322
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Pred. No. 5.11e-27;
0; Mismatches 9;
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                                              Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                         /organism-"Mus musculus"
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/lab_host="DH108"
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                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                          /strain="C57BL/6J"
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Best Local Similarity 84.2%;
Matches 48; Conservative
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:247664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA139013 320 bp mRNA EST 02-DEC-1996 mr04e06.rl Soares mouse 3NbMS Mus musculus cDNA clone 596434 5' AA139013
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Vartebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH108 (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 175;
Pred. No. 7.53e-39;
                                                                                                                                                                Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
                                                                                   mouseest@watson.wustl.edu
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Bost Local Similarity 76.7%;
Matches 102; Conservative
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        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 266)
3 (bases 1 to 266)
4 (bases 1 to 26)
5 (bases 1 to 26)
5 (bases 2 to 26)
5 (bases 3 to 26)
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                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-1995
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 266)
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Stretch_removed: removed at sequence 5'end
Normalization_method: Bento Soares, P.N.A.S in press;
Genexpress_library_idt: C;
Genexpress_sequence_idt: alc-07h08.
Location/Qualifiers
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partial cDNA sequence; transcribed sequence fragment.
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                                                                                                            Length 279;
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                                  5 others
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                                                                                                                                                               8; Indels
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H. sapiens partial cDNA sequence; clone c-07h08.
F01610
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Primer: (-21)M13_universal;
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Pred. No. 4.59e-05;
                                                                                                                                  1. No. 1.48e-14;
Mismatches 8
                                                                                                              82;
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/dev_stage="3 months old"
47 c 49 g 75 t
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                                                                                                            Score 31;
Pred. No.
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larity 82.7%;
Conservative
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Best Local Similarity 80.0%;
Matches 32; Conservative
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                                                                                                            Query Match
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Direct Submission
Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France
and Genetique Moleculaire et Biologie du developpement, CNRS UPR420
B.P. 8, 94801 Villejuif Cedex France. E-mail:
2 (bases 1 to 337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
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(Dases 1 to 337)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
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Normalization_method: Bento Soares, P.N.A.S. 91:9228-9232(1994);
Generalization_filt: C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N92UlO 358 bp mRNA EST 04-APR-1996 2a2lall.rl Homo sapiens cDNA clone 293180 5' similar to gb:M10942_cds1 Human metallothionein-Ie gene (HUMAN);. N92010
                    21-SEP-1995
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                                                                                                                                                                                     Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 337)
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/clone_lib="normalized infant brain cDNA from
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95277534
                                                                                                                     partial cDNA sequence; transcribed sequence fragment
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HSC3LC012 337 bp RNA EST
H. sapiens partial cDNA sequence; clone c-3lc01.
F10881
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CDNA sequence complementary to mRNA (3'end)
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Pred. No. 4.59e-05;
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/dev_stage="3 months old"
78 c 92 g 64 t
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Location/Qualifiers
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Best Local Similarity 69.4%;
Matches 43; Conservative
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AUTHORS
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Eutergonala; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterggil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 395)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
                                                                                                                                                                                     Deuterostomia; Chordata; Vertebrata; Grathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.

(bases 1 to 358)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hultmn,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (lift@@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                         Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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Pred. No. 4.59e-05;
0; Mismatches 11; Indels
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yj37c07.rl Homo sapiens cDNA clone 150924 5'.
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Best Local Similarity 75.6%;
Matches 34; Conservative
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/note="Organ: heart; Vector: pT713D (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCOTSGAGGGGGGGGGTGTTTTTTTTTTTTTTTTTT] double-stranded cDNA was size selected, ligated to Eco RI
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1099 Std Error: 0.00
Seg primer: mob.REGA+ET.
                                                                                                                                                                                                                                                                                                                                                                                      High qulity sequence stops: 314
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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2491f06.s1 Soares fetal heart NbHH19W Homo sapiens CDNA clone
W84628
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Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                      WashU-Merck EST Project
WashIngton University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                 Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
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WashU-Merck EST Project
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95 c
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Best Local Similarity 80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Conservative
                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
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adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pr773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19w."

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/dev_stage="19" weeks"
/lab_host="DH10B (ampicillin resistant)"
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Owery Match

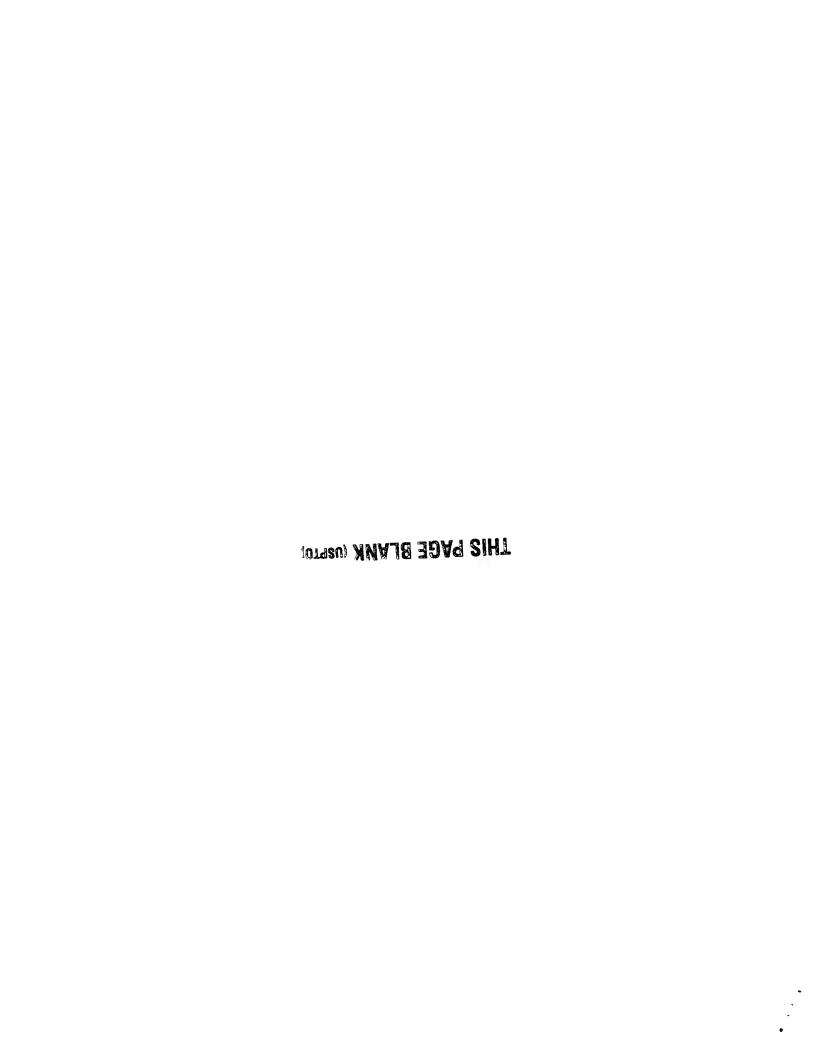
Query Match

Query Match

43; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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Db 326 ct 327 | 1 | Cp 589 CT 588 | Search completed: Thu Aug 21 13:59:38 1997 | Job time : 2124 secs.

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5.88e-54 2.88e-54 2.88e-54 2.02e-28 2.02e-28 3.02e-28 8.38e-27

G06794 MM1142620 AA185611 AA185611 AA128314 AMAA23834 AMAA23834 AA139013 AMA139075 MMAA84020 AA184020 AA184020 AA184020 AA184020 AA184020 AA184020

human STS WI-7983

DB

Length

Match

Score

No.

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	(TA)
Release 2 Copyright D	e 2.1D John F. Collins, Biocomputing Research Unit. ght (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a. Run on: Tabular output no	• n.a. database search, using Smith-Waterman algorithm Thu Aug 21 14:00:02 1997; MasPar time 343.89 Seconds 1028.472 Million cell updates/sec
Title: Description: Perfect Score: N.A. Sequence: Comp:	>US-08-320-157-8 (1-1287) from USO8320157.seq 1287 1 TITTAATATAAAATGTGCCTCAAGAGTACAGAAGCTT 1287 AAAATTATATATATAACACGGAGTTCTCATGCTTCGAA
Scoring table:	TABLE default Gap 6
Nmatch STD:	Dbase 0; Query 0
Searched:	359085 segs, 137405154 bases x 2
Post-processing:	Minimum Match 0% Listing first 45 summaries
Database:	EST-STS-THREE 1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204. 7:EST205 8:ESST206 9:EST207 10:EST208 11:EST209 12:EST210 13:EST201 14:EST212 15:EST213 16:EST214 17:EST215 18:EST212 14:EST212 15:EST213 16:EST214 17:EST215 23:EST221 24:EST222 25:EST223 26:EST224 27:EST225 23:EST221 24:EST222 25:EST223 26:EST224 27:EST225 24:EST221 24:EST222 25:EST223 26:EST224 27:EST235 23:EST231 34:EST232 35:EST233 36:STS1 37:STS2 38:STS3 46:EST314 47:ETS2 48:STS3 36:STS3 37:EST2 38:STS3 46:EST31 47:ETS2 24:EST3 36:EST23 36:STS10 49:GREST1 50:GREST2 51:GREST3 52:GREST4 53:GREST5 54:GREST5 55:GREST7 56:GREST3 57:GREST4 53:GREST5 54:GREST5 65:GREST7 56:GREST18 67:GREST24 73:GREST25 74:GREST5 80:GREST17 66:GREST2 77:GREST2 83:GREST3 75:GREST5 80:GREST1 66:GREST1 86:GREST3 88:GREST4 75:GREST5 80:GREST1 66:GREST1 87:GREST3 88:GREST4 75:GREST5 80:GREST1 61:GREST2 77:GREST3 88:GREST9 84:GREST2 80:GREST1 61:GREST2 77:GREST3 88:GREST1 75:GREST2 80:GREST1 61:GREST2 77:GREST3 88:GREST1 75:GREST2 80:GREST2 10:GREST1 77:GREST2 97:GREST3 84:GREST2 80:GREST2 10:GREST1 77:GREST2 97:GREST3 75:GREST2 80:GREST2 10:GREST2 77:GREST2 97:GREST3 85:GREST2 80:GREST2 10:GREST2 77:GREST2 97:GREST2 97:GR
Statistics:	Mean 11.601; Variance 2.220; scale 5.227

8.38 1.07e-07

> N97744 AA138853 MMAA89753

AA198152 N59408 AA126907 AA191208 AA115608 AA115474 N58693 G14786

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RESULT 1
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G06794
1258 bp DNA STS 19-OCT-1995
ACCESSION
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SURVE
SURVEDS
STS sequence; primer; sequence tagged site.
Human STSs derived from sequences in dbEST and the Unique collection.
ORGANISM Homo sapiens
ELKATYOTAE: mitochondrial eukaryotes; Metazoa; Chordata;
Homo sapiens
Collection.
ORGANISM Homo sapiens
TEKEPATOGA: Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Tetrapoda; Anniota; Mammalia; Theria; Eutheria; Primates;
Tetrapoda; Anniota; Mammalia; Theria; Eutheria; Primates;
TILLE
Whitehead Institute/MIT Center for Genome Research; Physically
COMMENT
CONTENT: The Mapped ESTS
UDUNIAL Unpublished (1995)
COMMENT
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

score g

Pred.

SUMMARIES

% Query

Result

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zq10f12.rl st zr77f05.rl so mt62e08.rl S

AA121520 AA182287 BM4163 AA197101 AA250729 MMAA85558

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Human brain cDNN (fet zol2h07.sl Stratagene human STS SHGC-10121.mz84f08.rl Soares mou mz84f08.rl Soares mou mz84f08.rl Soares mou mz84f08.rl Soares mou properties and stratagene stratagene stratagene stratagene mt. 7612.rl Soares mou RRAWGA12755K Brugia m

HUMSUPY306 AA130593 G14445 MM1171296 AA254866 N97957 G211837 AA224645 CPAA24645

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MMAA31246

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281..625
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942_A_12; 808_G_6,11,"
6 a 356 c 355 g 301 t 10 others
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21-FEB-1997 (Rel. 51, Created)
22-FEB-1997 (Rel. 51, Last updated, Version 2)
mt62e08.rl Soares 2NMT Mus musculus cDNA clone 634454 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN.;
                                                                                                                                                                                                                                                                                                                                        Prepared with primer pairs derived from U16811 -- Unigene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 94; DB 38; L
Pred. No. 5.87e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                0.025 units/ul
                                     Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 2
MM1142620 standard; RNA; EST; 133 BP.
AA185611;
                                                           Primer A: CIGATAACTIGGGGAGGCAA
                                                                     Primer B: GAGAGTCCAACTGCAAAGGC
STS size: 345
PCR Profile:
                                                                                                                              Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1.1258
                                                                                                                                                                                                        ğ
                                                                                                                                                                                         Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
                                                                                                                                                                                                                                                                          MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
                                                                                                                                                                                                                             Taq Polymerase:
Total Vol: 20 ul
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Best Local Similarity 95.4%;
Matches 104; Conservative
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                                                                                                          Presoak:
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by Dr. Bertrand Jordan. Library went through two round normalization, and was constructedby Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ccgtccccttctggacagcaggttgcccatgacacagaggaggtctttcgaagctacgta 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 Tel: 314 286 1800 Fast: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:386446 Trace considered overall poor quality Possible reversed clone: similarity sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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/dev_stage="4 weeks"
/lab_host="DH108"
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                                                                                                                            "The WashU-HHMI Mouse EST Project";
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COMMENT

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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,R., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA123834 310 bp mRNA EST 21-NOV-1996
mp93c04.r1 Soares 2NbMT Mus musculus cDNA clone 576774 5' similar
to TR:G595926 G595926 BAK-2 PROTEIN. ;.
Contact: Marra M/Mouse EST Project
WashU HHMI Mouse EST Project
WashU HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Pred. No. 2.88e-54;
0; Mismatches 16; Indels
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="634454"
/clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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/lab_host="DH10B"
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Best Local Similarity 81.6%;
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Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                    WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
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/clone_lib="Soares 2NbMT"
                     Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                         Email: mouseest@watson.wustl.edu
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Best Local Similarity 81.6%;
Matches 71; Conservative
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Best Local Similarity 78.2%;
Matches 104; Conservative
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                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:351422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1996 (Rel. 50, Created)
19-FBB-1997 (Rel. 51, Last updated, Version 2)
19-FBB-1997 (Rel. 51, Last updated, Version 2)
19-FBB-1997 (Rel. 5NDMT MUS musculus CDNA clone 576774 5' similar
10-TR-(5595926 G595926 BAR-2 PROTEIN. ;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                  Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                        /strain-"C57BL/6J"
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Similarity 78.2%;
104; Conservative
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Best Local Simile
Matches 104; (
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BASE COUNT
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and Eco RI sites of the modified pT7T3 vector. RNA provide
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mp3c04.r1 Soares 2NbMT Mus musculus cDNA clone 576774 5' similar
AA123834
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                           Seq
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royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:351422 primer: -28M13 rev2 from Amersham.
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Sequence 310 BP; 72 A; 96 C; 86 G; 55 T; 1 other;
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0; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="576774"
/clone_lib="Soares 2NbMT"
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WashU-HHMI Mouse EST Project
                                                                                                                                          /organism="Mus musculus"
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/dev_stage="4 weeks"
                                                                       Location/Qualifiers
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Galsel,S., Kucaba,T., Lacy,M., Lac,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZZO617 331 bp mRNA EST 10-FEB-1997 my25f11.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA clone 696909 5'.
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   This clone is available royalty-free through LLNL; contact the IMAGE consortium (info@image.llnl.gov) for further information. MGI:361866 Seg primer: -28MI3 rev2 from Amersham.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Pred. No. 8.38e-27;
0; Mismatches 9;
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/clone_lib="Soares mouse 3NbMS"
/sex="male"
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                                                                                                         /organism="Mus musculus"
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/dev_stage="4 weeks"
/lab_host="DH108"
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Marra,M. Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:351422
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Pred. No. 2.02e-28;
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                                                  Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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/dev_stage="4 weeks"
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Best Local Similarity 78.2%;
Matches 104; Conservative
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Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
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13-FEB-1997 (Rel. 50, Created)
13-FEB-1997 (Rel. 50, Last updated, Version 1)
my28fil.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 8.38e-27;
......tches 9; Indels
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/lab_host="DH10B"
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/lab_host="DH10B"
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Best Local Similarity 84.2%;
Matches 48; Conservative
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by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson
Waterston R.;
"The WashU-HHMI Mouse EST Project";
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19-FEB-1997 (Rel. 51, Last updated, Version 1)
mt22d08.rl Soares mouse 3NbMS Mus musculus cDNA clone 621807
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                                                                     Length 331;
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                                            DB 108; Len. 8.38e-27;
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mRNA <1..>331
Sequence 331 BP; 78 A; 104 C; 89 G; 60 T; 0 other;
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                                                              Score 39; DB 1C
Pred. No. 8.38e-
0; Mismatches
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/strain="C57BL/6J"
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/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>475
                                                                                                                                                                                                                                                                                   standard; RNA; EST; 475
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                                                                3.0%;
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SOURCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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DEFINITION

ACCESSION NID

KEYWORDS

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l (bases 1 to 475)
Marram M. Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The Washu-HMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loases 1 to 228)

Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Comman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E.
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2149C3 czapPFDd2.1, Debopam Chakrabarti Plasmodium falciparum cDNA
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                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Washu HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Seq primer: -28Ml3 rev2 from Amersham
High quality sequence stop: 438.
Location/Qualifiers
1.475 "... musculus"
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Best Local Similarity 76.0%;
Matches 38; Conservative
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   Mus musculus
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AUTHORS
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                    AA184020 475 bp mRNA EST 17-FEB-1997 mt22d08.rl Soares mouse 3NbMS Mus musculus cDNA clone 621807 5' AA184020
                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone="611807"
/clone_lib="Soares mouse 3NbMS"
/sex="male"
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.07e-07;
0; Mismatches 12; Indels
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High quality sequence stop: 438.
Location/Qualifiers
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/dev_stage="4 weeks"
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Best Local Similarity 76.0%;
Matches 38; Conservative
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source

FEATURES

RESULT 13 DEFINITION ACCESSION

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BASE COUNT

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Search completed: Thu Aug 21 14:17:25 1997 Job time: 1043 secs.
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Bukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa; Bukaryotae; mitochondrial eukaryotes; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 289)

2 Dame, J. B., Arnot, D. E., Bourke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Cowman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J. Y., Reddy, G. R., Rubio, J., Schuster, S. M., Su, X.-Z., Thompson, J. K., Vital, F., Wellems, T. E. and Werner, E. Current status of the Plasmodium falciparum genome project

E 97001675
                                                                                                                                                                                                                                                                                                                                                         /note="Vector: Lambda ZAP II; Site_1: ECOR I; Site_2: Xho I; PolyA+ RNA, from asynchronous blood stage parasites of the Dd2 isolate cultured in vitro, was reverse transcribed using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. ECOR I adapters were ligated to the CDNA, and it was digested with Xho I. Prepared fragments were ligated into ECOR I + Xho I digested lambda ZAP II vector."

/clone="PF2149c" / Lobopam Chakrabart!"
/lab_host="E. coli XL-1 blue"
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bd2.1, Debopam Chakrabarti Plasmodium falciparum cDNA
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Current status of the Plasmodium falciparum genome project
Mol. Blochem. Parasitol. 79, 1-12 (1996)
97001675
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Pred. No. 3.33e-05;
0; Mismatches 20; Indels
                                                                                            Contact: Debopam Chakrabarti
Department of Molecular Biology and Microbiology
University of Central Florida
Orlando, FL 32816-236
Tel: 407 384 205
Fax: 407 384 305
Email: dchak@pegasus.cc.ucf.edu
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                                                                                                                                                                                                                                                                                                                                         /strain="Dd2"
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Bost Local Similarity 68.8%;
Matches 44; Conservative
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clone PF2232C.
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/note="Vector: Lambda ZAP II; Site_1: EcoR I; Site_2: Xho I; PolyA+ RNA, from asynchronous blood stage parasites of the Dd2 isolate cultured in vitro, was reverse transcribed using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were ligated to the cDNA, and it was digested with Xho I. Prepared fragments were ligated into EcoR I Xho I digested lambda ZAP II vector."
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/lab_host="E. coli XL-1 blue"
<1..>289
                                                                                                                                                                                                                                                                                                                                                                                                            1 others
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Pred. No. 1.98e-06;
0; Mismatches 25; Indels
                                            /organism="Plasmodium falciparum"
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Location/Qualifiers
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Best Local Similarity 66.7%;
Matches 50; Conservative
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Biocomputing Research Unit.

University of Edinburgh, U.K. t (c) 1993, 1994, 1995 University of Edinbu. Distribution rights by IntelliGenetics, Inc. Release 2.1D John F. Collins, Copyright

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Aug 20 11:04:54 1997; MasPar time 5.42 Seconds 445.465 Million cell updates/sec Run on:

not generated. Tabular output

Description: Perfect Score:

>US-08-320-157-9 (1-211) from US08320157.pep 1554

1 MASGQGPGPPRQECGEPALP.....LVVLGVVLLGQFVVRRFFKS 211

PAM 150 Gap 11 Scoring table:

Sequence:

96640 segs, 11439865 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 a-geneseq27 Database:

scale 0.230 Mean 32.557; Variance 141.390; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	8.16e-138	8.16e-138	2.32e-135	2.32e-135	2.32e-135	6.78e-97	1.38e-89	5.18e-72	9.24e-15	2.11e-14	8.96e-14	8.96e-14	1.35e-13	1.35e-13	2.04e - 13	2.04e-13	2.04e-13	2.04e-13	2.04e-13	2.04e-13
Description	Bak-2 protein.	Human Cdn-2.	Human Cdn-1.	Bak protein.	Bcl-Y apoptosis-relat	Human Cdn-1(60-211).	Human Cdn-1(71-211).	Human Cdn-1(96-211).	Apoptosis-blocking pr	Chicken lymphoid BCL-	Human thymus BCL-XL.	Bcl-XL protein.	Apoptosis-blocking pr	Apoptosis-blocking pr					oncode	Sequence of bcl-2-alp
ID	W03669	R77877	R77876	W03668	R81451	R77879	R77880	R77881	W01020	R68884	R68887	W05821	W01019	W01018	R71405	R68886	R70332	R71404	R47344	P80987
DB	20	13	13	20	17	13	13	13	13	13	13	20	13	13	13	13	13	13	σ	Н
Length	211	211	211	211	211	152	141	116	232	190	233	233	232	239	205	205	202	239	239	239
Query	100.0	100.0	98.4	98.4	98.4	73.1	68.3	9.99	17.7	17.4	17.0	17.0	16.9	16.9	16.7	16.7	16.7	16.7	16.7	16.7
Score	1554	1554	1529	1529	1529	1136	1061	880	275	271	264	264	262	262	260	260	260	260	260	260
Result No.	1	7	m	4	ស	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20

2.04e-13	2.04e-13	9.35e-11	4.71e-10	8.62e-10	2.88e-09	7.82e-09	1.34e-06	3.61e-05	7.02e+00	9.81e+00	1.16e+01	1.16e+01	1.16e+01	1.37e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	1.61e+01	3.09e+01	3.09e+01	3.09e+01	3.09e+01
Human bcl-2 protein.	Bcl-2 oncogene produc	Sequence of bcl-2-bet	Apoptosis-blocking pr	•	Human Cdn-3.		Human mcl-1 gene prod	Human thymus BCL-X1,	Deduced sequence enco	Human thymus BCL-XS.	Human IFG-1 receptor.	type	IGF-1 receptor.	Duffy blood group gpD	Soybean chlorotic mot	IGF-I receptor 957A v	-I receptor	IGF-I receptor 1003A	IGF-I receptor 943A v	IGF-I receptor.	ACT-4-h-1 receptor se	Insecticidal protoxin	Peripheral nervous sy	nervous
R70331	R42312	P80988	W01021	R71407	R77878	R71406	R68814	R68885	R76996	R68888	R60795	R91429	R95244	R73955	R11516	R63125	R63124	R63126	R63123	R63122	R79904	R48678	R99639	R92317
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16.7	٠	14.8	14.3	14.1	13.7	13.4	11.7	10.6	6.3	6.2	6.1	6.1	6.1	0.9			0.9	•	•		5.7	5.7	5.7	5.7
260	260	230	222	219	213	208	182	165	86	96	95	95	92	94	66	93	93	93	93	66	88	83	83	68
21	22	23	24	25	26	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42		44	45

ALIGNMENTS

protein

Sisclosure; Fig 2: 24pp; English.

This Bak-2 protein sequence represents a bcl-1 homologue which
interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1

Enteracts with Epstein-Barr virus (EBV) early lytic cycle BHRF1

Enteracts with Epstein-Barr virus (EBV) early lytic cycle BHRF1

Enteracts with Epstein-Barr virus (EBV) early lytic cycle BHRF1

Enteracts and is capable of modulating apoptosis. The protein may protein, in a new virucide drug screening method, which involution of Bak-2 protein and a viral protein (e.g. EBV BHRF1).

Exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELSA. Interaction of Bak-2 and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or N-PSDB; 742139. Screening for anti-viral agents - by detecting the ability of an agent to disrupt the interaction of a Bak protein and a viral Bak-2 protein. Haman; Bak-2; apoptosis; latency; virus replication; Bak-2; apoptosis; latency; virus replication; Epstein-Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; immunoassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic. WO9633416-A1. ¥ 24-0CT 1996. 19-APR-1996; U05639. 20-APR-1995; US-426529. (LXRB-) LXR BIOTECHNOLOGY INC. RESULT 1 ID W03669 standard; Protein; 211 22-FEB-1997 (first entry) Barr PJ, Kiefer MC; WPI; 96-485886/48. 211 AA; diagnostic agents Sequence W03669;

ö 0; Gaps Score 1554; DB 20; Length 211; Pred. No. 8.16e-138; 0; Mismatches 0; Indels 0 ch 1 Similarity 100.0%; 211; Conservative Query Match Local Best Loca Matches

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vtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiasslfe
          sginwgrvvallgfsyrlalhiyqrgltgflgqvtrfvvdfmlhhciarwiaqrggwvaa
                                               masgqgpppprqecgepalpsaseeqvaqdteevfrsyvfyhhqqeqeaegaaapadpem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema. Homo sapiens.
                                                                                                                                                                  Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema. Homo sapiens. W09515084-A.
                                                                                                                                                                                                                                                                                                                                          Cdn-2 CDNA was isold. from a human placental genomic library using a 950 bp fragment of Cdn-1 CDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (R77876).
Sequence 211 AA;
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Pred. No. 8.16e-138;
0; Mismatches 0;
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                                                                                                                                                                                                                            30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTEGINOLOGY INC.
Barr PJ, Klefer MC;
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R77877 standard; Protein; 211
R77877;
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Local Similarity 100.0%;
es 211; Conservative
                                                                                                                                                    (first entry)
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WPI; 95-215106/28.
N-PSDB; Q95493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; 095492.
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 masgqgpgpprqecgepalpsaseeqvaqdteevfrsyvfyrhqqeqeaegvaapadpem 60
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                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig. 3A-B; 66pp; English.

Cdn-1 CDNA was isolated from a human heart CDNA library using a previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HT29 cells. Expression of cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
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Epstein-Barr Virus; BHRF1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1529; DB 13; Length 211;
Pred. No. 2.32e-135;
5; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
Disclosure; Fig 1; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 4
W03668 standard; Protein; 211
                                                                                                                 (LXRB-) LXR BIOTECHNOLOGY INC.
Barr PJ, Kiefer MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.4%; silarity 97.2%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-1996; U05639.
20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY
Barr PJ, Kiefer MC;
                                                          30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barr PJ, Kiefer M
WPI; 96-485886/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 AA;
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WO9633416-A1.
08-JUN-1995.
30-NOV-1994;
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
                                                                                                                                                                Human Cdn-1(60-211)
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                                                                                                                                                                                                             Homo sapiens.
WO9515084-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
WO9515084-A.
                                                                                                                                                    21-NOV-1995
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                                                                                                                                                                                                                                     08-JUN-1995
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Matches
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                                                                                                                                              61 vtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiatslfe 120
                                                                                                                                                         61 VILPLOPSSTMGOVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFE 120
                                                                                                                                                                                                        61 vtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiatslfe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human Bcl-Y protein - used to develop prods. for treating disorders characterised by inappropriate cell proliferation or cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 4; 100pp; English.

Bcl-Y protein (R81451) is a member of the Bcl-2 family and can induce apoptosis in cells and function as a negative regulator of Bcl-2 function. Bcl-Y mRNA was detected in all human tumour cell lines examined and is also widely expressed in primary human tissues. It can be obtd. by expression of a full-length cDNA clone (T17375) in pref. mammalian host cells. Bcl-Y can be used to develop prods. for treating disorders associated with inappropriate cell proliferation or cell death, and to raise antibodies used for
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                   1 masgggpppprqecgepalpsaseeqvaqdteevfrsyvfyrhqqeqeaegvaapadpem
replication or latency in the absence of apoptosis. Compounds inhibit the interaction may be used as virucide, antitumour or
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                BCl-Y apoptosis-related protein.
BCl-Y; apoptosis; cell proliferation; cell death; diagnosis;
                                                         Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                               Indels
                                                        Score 1529; DB 20;
Pred. No. 2.32e-135;
5; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                   /label- C-terminal_domain
/note- "putative membrane localisation sequence"
WO9605232-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the diagnosis or monitoring of such disorders
                                                                                                                                                                                                                                          181 Inlgngpilnvlvvlgvvllggfvvrrffks 211
                                                                                                                                                                                                                                                      181 LNLGNGPILNVLVVLGVVELLGQFVVRRFFKS 211
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
188..205
                                                                                                                                                                                                                                                                                                 .T 5
R81451 standard; Protein; 211 AA.
                                                      Query Match
Best Local Similarity 97.2%;
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                    02-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FFB-1996.
09-AUG-1995; U10103.
09-AUG-1994; US-287427.
11-CCT-1994; US-321071.
(IMMU ) IMMOUNGEN INC.
Chittenden ID;
WPI: 96-139648/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 AA;
                      diagnostic agents
Sequence 211 AA
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                                    Seguence
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Sginwgrvvallgfgyrlalhvyghgltgflgqvtrfvvdfmlhhciarwiaqrggwvaa 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           esginwgrvvallgfgyrlalhvyghgltgflggvtrfvvdfmlhhciarwiagrggwva 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MBIR DJ. Kiefer MC; WPI; 95-215106/28.
WPI; 95-215106/28.
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etc.
Disclosure; Fig.11; 66pp; English.
Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Ras-mediated apoptosis. Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly decreased this activity, suggesting that small, truncated Cdn-1 molecules may be potent therapeutics.
Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                     Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
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30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
BALT PJ. Klefer MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                          77 6
R77879 standard; Protein; 152
R77879;
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                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             shock; lymphoma; eczema
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potent the Sequence

Query Match

Matches

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neuronal cells, lymphocytes and cancers
Claim 4; Page 87; 127pp; English.
Claim 4; Page 87; 127pp; English.
This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures.
The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases
                                                                                                                                                                                                                                                                                             Chinadural G;

WPI; 96-427055/43.

WPI; 96-427055/43.

WPI; 96-427055/43.

WPI; 96-427055/43.

WINCIALC acids encoding apoptosis regulating proteins - useful for diagnosing and treating immune disorders, malignancies, etc.

Example 8; Page 34-35; 60pp; English.

CC The 80-6 mutant (W01020) of the bcl-2 oncogene product (W01018)

CC lacks amino acids 80-86 of the native protein. This and other

CC lacks amino acids 80-86 of the native protein. This and other

CC commine the interactions between Bcl-2 and novel apoptosis-

CC commine the interactions between Bcl-2 and novel apoptosis-

CC camine the interactions defined that are essential for interaction with the Nip proteins. These motifs show homology

CC interaction with the Nip proteins. These motifs show homology

CC apoptosis-blocking protein (W01010).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 ffssgpghtphpaasr-dpvartsplgtpaapgspvppvvhltlrgagddfsrryrrdfa 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 emssqlhltpftargcfatvveelfrdgvnwgrivaffefggvmcvesvnremsplvdni 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 TMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVALLGFSYRLALHIYQRGLTGFLGQV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurodegenerative disease; autoimmune disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g
                     18-DEC-1996 (first entry)
Apoptosis-blocking protein Bcl-2 mutant 80-6 (del80-86).
Apoptosis-regulating protein; Bcl-2; oncogene;
adenovirus ElB 19K protein; cell death; cancer; tumour;
immune disorder; diagnosis; therapy; Bipla; Bipl3; Bip5; NIp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amylotrophic lateral sclerosis; multiple sclerosis; oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New poly-nucleotide encoding new poly-peptide(s) that modify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicken lymphoid BCL-X.
Chicken; bird; fowl; BCL-X; apoptosis; cell death; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 275; DB 19; Length 23
Pred. No. 9.24e-15;
41; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 alwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : ::::: | : | | : | | | :| | | : | | 15 TRFVVDFMLHHCIARWIAQRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
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22.0UN-1993; US-081448.
(ARCH) ARCH DEV CORP.
(UMXI ) UNIV MICHIGAN.
BOISE LH, NUNEZ G, Th
                                                                                                                                                                                                             25-SEP-1996,
21-MAR-1996, 104542,
21-MAR-1995, US-408095,
(UYSL-) UNIV ST LOUIS.
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WPI; 95-052079/07.
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                                                                                                                                          Nip2; Nip3.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 MLQHLQPTAENAYEYFTKIASSLFESGINWGRVVALLGFSYRLALHIYQRGLTGFLGQVT 155
                                                                                                                                                                                                                                                                                                                                                                                                                       71 MGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVA 130
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                        related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure: Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Truncated Cdn-1 derivatives given in R77879-81 were used to test the effects of deleting the N-terminal sequences of Cdn-1
                                                                                  Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 70 amino acids of Cdn-1 improved this activity, suggesting that small, truncated Cdn-1 molecules may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequences encoding Cdn apoptosis modulators - and
nucleic acid sequences encoding Cdn apoptosis modulators - and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
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                                                                                                                                                                                                                                                                                 Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.6%; Score 880; DB 13; Length 116; Larity 96.6%; Pred. No. 5.18e-72; Conservative 4; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                               Score 1061; DB 13;
Pred. No. 1.38e-89;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W01020 standard; Protein; 232 AA.
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
Barr PJ, Klafer MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 vlvvlgvvllggfvvrrffks 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 VLVVLGVVLLGQFVVRRFFKS 211
                                                                                                                                                                                                                                                                            / Match 68.3%;
Local Similarity 97.2%;
Nes 137; Conservative
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ses 112; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 AA;
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WO9515084-A.
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Sequence Query Match

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N-PSDB; T40079
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EP-733706-A2.
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WO9634956-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 maavkqalreagdefelryrrafsdltsqlhitpgtayqsfeqvvnelfrdgvnwgriva 142
                                                                                                                                                                                                                                                                                                                                         130 gvnwgrivaffsfggalcvesvdkemrvlvgrivswmttyltdh-ldpwigenggwvrta 188
                                                                                                                                                                                                                                                                                                                                                                                70 slevheivrasdvrgalrdagdefelryrrafsdltsglhitpgtaygsfegvvnelfhd 129
                                                                                                                                                                                                                                                                                 62 TLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFES 121
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Human; bcl-XL; T-lymphocyte; cell death; BH1 domain; BH2 domain;
Bcl-2 homology domain; gene therapy; HIV; AIDS; antisense;
immune disorder; autoimmune disease; graft rejection;
(premature PCD), e.g. Parkinson's disease, amylotrophic lateral sclerosis and multiple sclerosis.
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Pred. No. 8.96e-14;
37; Mismatches 46; Indels
                                                                                                                Length 190;
                                                                                                          Score 271; DB 13; Length 19
Pred. No. 2.11e-14;
36; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 11
R68887 standard; Protein; 233 AA.
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Best Local Similarity 28.0%;
Matches 33; Conservative
                                                                                                          Match 17.4%;
Local Similarity 28.1%;
les 34; Conservative
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30-MAR-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-1994; U07089, 22-JUN-1993; US-081448. (ARCH-) ARCH DEV CORP. (UNMI ) UNIV MICHIGAN.
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                                                        Seguence
                                                                                                                Query Match
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                                                                                                                                                                   Matches
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Inducting or preventing death of T cells by bcl-XL protein regulation or preventing death of HIV infected cells or to down:regulate immune responses in immune diseases

Tused to increase survival of HIV infected cells or to down:regulate immune responses in immune diseases

Disclosure; Page 52-53; 76p; English.

This is the sequence of a human bcl-XL protein, which protects

Thymphorytes against cell death. A splice variant form, bcl-XS, lacks a stretch of 63 amino acids, and is a dominant negative regulator of bcl-XL function. The gene may be modified to facilitate interaction with antagonistic Bad protein, by modification of the Bcl-2 homology domains BHI and/or BHZ. The bcl-XL gene may be introduced into T-cells in vivo or ex vivo via gene transfer using a vector for HIV infection gene therapy, to augment intracellular bcl-XL protein levels and protect from cell death. A corresponding therapy of e.g. autoimmune disease, graff rejection or graft-versus-host disease, to induce cell death (e.g. apoptosis) and down-regulate the immune response in a T-lymphocyte population.
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Example 8; Page 33-34; 60pp; English.
The 42-8 mutant (W1019) of the bcl-2 oncogene product (W01018)
lacks amino acids 42-48 of the native protein. This and other Bcl-2 mutants (see also W01020-21) were used in a two hybrid assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-1996 (first entry)
Apoptosis-blocking protein Bcl-2 mutant 42-8 (del42-48).
Apoptosis-regulating protein; Bcl-2; oncogene; adenovirus BlB 19K protein; cell death; cancer; tumour; immune disorder; diagnosis; therapy; Bipla; Bipl3; Bip5; NIP1;
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graft-versus-host disease; apoptosis; adoptive immunotherapy \ensuremath{\mathsf{Homo}} sapiens.
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Pred. No. 8.96e-14;
                                                                      Location/Qualifiers
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W01019 standard; Protein; 232 AA.
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Best Local Similarity 28.0%;
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                                                                                                       129..148
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                                                                                                                                                                                                                                                                                                                                                                                                                  (ARCH-) ARCH DEV CORP.
(USNA ) US SEC OF NAVY.
June CH, Thompson CB;
                                                                                                                                                                                                                                                                                                                                               04-MAY-1995; US-435518.
07-JUN-1995; US-481739.
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02-MAY-1996; U06203.
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                                                                                                                                                                                                       "BH2 domain"
                                                                                                                                        "BH1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chinnadurai G;
WPI; 96-427055/43.
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WPI; 96-506159/50.
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132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190
                                                              191 dnggwdafvel-ygpsmrpl
                                                                                                                                                                                  Human bcl-2 beta protein
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25-MAY-1994; US-248819.
(UNIW ) UNIV WASHINGTON.
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                                                                                                                                                                                                                                                                                                                      /label- BH1_domain
                                                                                                                                                                                                                                                                                                                                                           /label- BH2_domain
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                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                  125 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 183
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                                                                                                                                                                                               tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargcfa 124
                                                                                                                                                                      Gaps
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Nucloic acids encoding apoptosis regulating proteins – useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosing and treating immune disorders, malignancies, etc.
Example 8; Page 32-33; 60pp; English.
The bcl2 oncogene product (W01018) enhances the survival of haematopoietic B and Teells by blocking apoptosis induced by diverse agents. Its activity is similar to that of the 19k portein (W01010) of adenovirus Elb 3 Novel proteins, Bipla, Bipl3 and Bip5 (W0100-02), that specifically interact with Bcl-2, have been identified. Mutational analysis (see also W0109-79) associate with Bcl-2 at specific sites (see also W0109-79) associate with Bcl-2 at specific sites (see also W01093-04) that show homology to motifs (W01005-06) on 19k.
                   regulating proteins Nipl, Nip2 and Nip3 (W00997'99). The Nip proteins were unable to interact with mutant 42-8. The site of deletion in this mutant corresponds to a motif (see also W01003) on Bcl-2 essential for interaction with Nip proteins. A second binding motif (W01004) of Bcl-2 was also identified, and both show homology to motifs (W01005-06) found on the 19K protein (W01010) of edenovirus ElB.
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Apotosis-blocking protein Bcl-2.
Apotosis-regulating protein: Bcl-2; oncogene;
adenovirus ElB 19K protein; cell death; cancer; tumour;
immune disorder; diagnosis; therapy; Bipla; Bipl3; Bip5; NIp1;
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examine the interactions between Bcl-2 and novel apoptosis-
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Pred. No. 1.35e-13;
37; Mismatches 57; Indels
                                                                                                                                             Length 232;
                                                                                                                                          Score 262; DB 19; Length 23:
Pred. No. 1.35e-13;
37; Mismatches 57; Indels
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/note- "interacts with Bip proteins"
EP-733706-A2.
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/note= "interacts with Bip proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   W01018 standard; Protein; 239 AA
                                                                                                                                                                                                                                                                                                     184 dnggwdafvel-ygpsmrpl 202
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173 QRGGWVAALNIGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.9%;
|larity 29.3%;
|Conservative
                                                                                                                                          / Match 16.9%;
Local Similarity 29.3%;
nos 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1996.
21-MAR-1996; 104542.
21-MAR-1995; US-408095.
(UYSL-) UNIV ST LOUIS.
Chinnadural G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 AA;
                                                                                                                   232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                   Sequence
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
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Wethods for producing and identifying mutant bcl-2 proteins -
that lack death repressor activity and/or lacks binding to Bax.

By Disclosure; Page 40; 139p; English.

The sequences given in R71404-05 represent the human bcl-2 alpha and beta proteins respectively. bcl-2 is encoded by a proto-oncogene and care apportens respectively. bcl-2 is encoded by a proto-oncogene and care apportens respectively. bcl-2 is encoded by a proto-oncogene and care apportens respectively. bcl-2 is encoded by a proto-oncogene and confined by enhancing the survival of hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated cytoplasmic protein and is thought to function by enhancing the survival of hematopoietic cell systems. bcl-2 has not been shown to directly promote cell cycle progression nor does it necessarily alter the dose reponse to limiting concentrations of IL-3. bcl-2 has been shown to form heterodimers with a 21 kD protein. Bax. overexpressed Bax accelerates apportence cell death induced by cytokine deprivation in an IL-3 dependent cell line, and it also acts to counter the death repressor activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines cell survival or death collowing an apoptotic stimulus. The invention gives a mutant form of bcl-2 in which there is at least one amino acid substitution or deletion collowing an apoptotic stimulus. The inventor protein substantially incapable of binding Bax and/or incapable of death effector molecules. Up regulating bcl-21s beneficial in treatment and diagnosis of immunodeficiency diseases, including Alba and securors.

Consumers and include and ischaemic cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ж
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
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4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation; cell cycle progression; Brotein; B cell; T cell; proliferation; cell cycle progression; Bax; apoptotic cell death; apoptosis; cytokine; death repressor; BH1; BH2; cancer theraph; hyperplasia; immunodeficiency disease; AIDS; neurodegeneration; isochemic cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>...</del> ...
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Pred. No. 2.04e-13;
37; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
136..155
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                                                                                                                                                                                                                                                                                                                     T 15
R71405 standard; protein; 205
R71405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 QRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h
Similarity 29.7%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1995 (first entry)
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113 KIASSLFESGINWGRVVALLGFSYRLALHIYQRGLTGFLGQVTRFVVDFMLHHCIARWIA 172 ò

191 dnggwyga 198 : ||||:| 173 QRGGWVAA 180 do Vy

Search completed: Wed Aug 20 11:05:16 1997. Job time : 22 secs.

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233 244 255 272 273 333 331 331 332 333 333 333 333 333 33	RESULT ID BCLX_CHICK AC Q07816; DT Q1-FEB-1995 DT	CC -1. SIMILARI DR EMBL, 223110 DR PIR, 44737; DR PRS, 4737; DR PRS, 223110 DR PRS, 223110 KW APOPTOSIS. SQ SEQUENCE 1 QUELY MATCH Best Local Simi Matches 34; Db 70 slevhei 1; Cy 62 TLPLOPS Db 130 gymwgri Db 130 gymwgri Db 130 gymwgri Cy 122 GINWGRV Db 189 1 189 QY 181 L 181 RESULT 2
***** lease Pyrig prote	Percett Score: (1-21) Irom USU832015/.pep Perfect Score: (1541) Irom USU832015/.pep Sequence: 1554 Sequence: 1564 Sequence: 1564 Sequence: 1562 Scoring table: PAM 150 Gap 11 Searched: 59021 segs, 21210388 residues Post-processing: Minimum Match 0% Listing first 45 summaries Database: swiss-prot34 Spart8 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part101:part11 Statistics: Mean 47.039; Variance 90.944; scale 0.517 Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Query No. Description Pred. No.

PRT; 233 AA.

STANDARD;

US-08-320-157-9.rsp

TRANSMEMBRANE; MITOCHONDRION

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APOPTOSIS;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
GALLIPORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maavkqalreagdefelryrrafsdltsqlhitpgtayqsfeqvvnelfrdgvnwgriva 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 MGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 ffsfggalcvesvdkemqvlvsriaswmatylndh-lepwiqenggwdtfvdlygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHOWN HERE) AND
                                                                                                                                          EUKARYOTA; METAZOA; CHÖRDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                     MICHABLIDIST,
MICHABLIDIST,
MICHABLIDIST,
L SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

1-1 FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.

1-1 ALTENNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE)
BCL-X(S), ARE DERIVED BY ALTERNATIVE SPLICING.

1-1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
R EMBL; X82537; G607178; -.
R EMBL; X82537; G607178; -.
W APOPTOSIS: ALTERNATIVE SPLICING.
T VARSPLIC 126 188 MISSING (IN BCL-X(S)).

SEQUENCE 233 AA; 26130 MW; E0589815 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 268; DB 1; Length 233;
Pred. No. 5.65e-29;
37; Mismatches 46; Indels
                01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
10-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE, 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D11382; G222794; -
EMBL; D11381; G222794; JOINED.
EMBL; Z11961; G62970; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 28.0%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                  RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A37332; A37332.
PIR; S24390; S24390.
PROSITE; PS01080; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 92379084.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL2_CHICK
Q00709;
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CELL 74.597-608(1993).

-1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH.

-1- ALTERNATIVE PRODUCTS: TWO ISOPORMS, BCX-X(L) (SHOWN HERE) AND BGL-X(S), ARE DERIVED BY ALTERNATIVE SPLICING.

-1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS TAAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING LONG-LIVED POSTMITUTOTIC CELLS, SUCH AS ADULT BRAIN.

-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

EMBL; Z23116; G513237; -.

BMBL; Z23116; G513901; -.

MIM; 600039; -.
                                                                                                                                                                                                                                                     60 hhrpeppgsaaasevppae-glrpapp-g-vhlalrqagdefsrryqrdfaqmsgqlhlt 116
                                                                                                                                                                                                                                                                                 117 pftahgrfvavveelfrdgvnwgrivaffefggvmcvesvnremsplvdniatwmteyln 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 maavkqalreagdefelryrrafsdltsqlhitpgtayqsfeqvvnelfrdgvnwgrlva 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 ffsfggalcvesvdkemqvlvsriaawmatylndh-lepwiqenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E -> S (IN REF. 2).
GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                      Length 233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOISE I.H., GONZALEZ-GARCIA M., POSTEMA C.E., DING L.,
LINDSTEN T., TURKA L.A., MAO X., NUNEZ G., THOMPSON C.B.;
CELL 74:597-608(1993).
                                                                                                                                                                  Score 266; DB 1; Length 233
Pred. No. 1.34e-28;
42; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 17.0%; Score 264; DB 1; Length 233 Local Similarity 28.0%; Pred. No. 3.16e-28; Pred. 37; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 188 MISSING (IN BCL-X(S)).
70 70 G -> A (IN G510901).
233 AA; 26049 MW; 57C67491 CRC32;
                                                               (IN REF. 2).
H -> T (IN REF. 2).
G -> V (IN REF. 2).
4; 3376502C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AA
      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 rh-lhnwiqdnggwdafvelygns 199
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VARSPLIC 126 188 MIS
CONFLICT 70 70 G -
                                                                                                                            25687 MW;
                                                                                                                                                                    Query Match
Best Local Similarity 28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
    228
64
82
                                                                                 121
139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN)
                                                                                                                            233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93364977
                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
BCLX_HUMAN
Q07817:
                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
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FRANSMEM
                 CONFLICT
                                         CONFLICT
                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                Matches
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PROTEIN BCL-2-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              э;
                                                                                                                                                                                                      132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                  -i- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
PARB, M19395; G173389; ALT_SEQ.
PIR: B29409; TV4U0B1.
                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01080; BCL2, PROSITE; PS01080; MEMBRANE; PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; MEMBRANE; MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
SEQUENCE 205 AA; 22311 MW; ED321E5E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.5%; Score 256; DB 1; Length 205; Best Local Similarity 29.7%; Pred. No. 9.72e-27; Matches 38; Conservative 35; Mismatches 51; Indels
                                                                                                                       TSUJIMOTO Y., CROCE C.M.;
PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL. 10, CREATED)
(REL. 25, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
                             01-MAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROTEIN BCL-2-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA
                 205 AA
                                                                                                                                                                EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                 PRT;
                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                 REVISIONS TO 96 AND 110
                                                                                                                                                                                          SUBCELLULAR LOCATION.
                                                                                                      SEQUENCE FROM N.A. MEDLINE; 86259760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 dnggwvga 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 QRGGWVAA 180
                                                                                                                                                        MEDLINE; 92375724
                                                                                                                                                                                                   MEDLINE; 91066924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC2A_HUMAN
P10415;
01-MAR-1989 (
01-APR-1993 (
01-NOV-1995 (
5
BC2B_HUMAN
P10416;
01-v
                                                                                                                                                                                                                                                                                                                                                                            MIM; 151430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
ID BC
AC P1
DT 01
DT 01
        RESULT
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HOCKERBERY D., WUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
NATURE 348:334-336(1990).
-!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDANT PACHWAY TO PREVENT APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDANT PACHWAY TO PREVENT APOPTOSIS AT SITES
OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
II CHRONIC LYMPHATIC LEGUREMIA) BY A CHROMOSOMAL TRANSLOCATION
IT CHRONIC LYMPHATIC LEGUREMIA) BY A CHROMOSOMAL TRANSLOCATION
IT CHRONIC LYMPHATIC LEGUREMIA) BY A CHROMOSOMAL TRANSLOCATION
IT (14.18) (032:021) WHICH INVOLVES BCLZ AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, AND PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-!- SINILARITY: BELOGS TO THE BCL-2 FAMILY.
EMBL, M13994; G179371; -.
EMBL, M13745; G179371; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE; MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 16.5%; Score 256; DB 1; Length 239; Local Similarity 29.3%; Pred. No. 9.72e-27; les 41; Conservative 37; Mismatches 57; Indels
                                                                                                                                                                                                       TSUJIMOTO Y., CROCE C.M.;
PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 59 P -> T (IN REF. 3).
117 117 S -> R (IN REF. 3).
239 AA; 26266 MW; 75084B59 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                              MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEARY M.L., SMITH S.D., SKLAR J.;
CELL 47:19-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 dnggwdafvel-ygpsmrpl 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 QRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                              REVISIONS TO 96; 110 AND 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 151430; -.
PROSITE; PS01080; BCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION. MEDLINE; 91066924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A29409; TVHUA1.
PIR; A24428; TVHUBC.
PIR; C37332; C37332.
                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 86259760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 87002488.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 9
BCL2_RAT
P49950;
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 9337574.

EQUCHI Y., EWERT D.L., TSUJIMOTO Y.;

EQUCHI Y., EWERT D.L., TSUJIMOTO Y.;

NUCLEIC ACIDS RES. 20:4187-4192[1992).

-1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDARY TO PREVEWE APOPTOSIS AT SITES OF FREE RADICAL GENERALION SUCH AS MITOCHONDRIA.

-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

-1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
                                                                                                                                                                                                                          1; Gaps
                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-LIVER;
BEDLINE; 87187643.
NEGRIN M., SILINI E., KOZAK C., TSUJIMOTO Y., CROCE C.M.;
CELL 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 251; DB 1; Length 199
Pred. No. 8.18e-26;
29; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APOPTOSIS; ALTERNATIVE SPLICING; MEMBRANE; MITOCHONDRION SEQUENCE 199 AA; 22299 MW; 3E60FA47 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwvga 195
                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             DIFFER AT THEIR C-TERMINAL ENDS.
-- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL. M15505 (3387110) -.
PIR; B25560; TWSB1.
PROSITE; PS01080; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 16.2%;
Local Similarity 31.1%;
108 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                  01-MAR-1989 (REL. 10,
01-MAR-1989 (REL. 10,
01-OCT-1996 (REL. 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS TO 221-222.
                                                                                                                MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE)
                                                                          PROTEIN BCL-2-BETA.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                87187643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
BC2A_MOUSE
P10417:
                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgr1vaffefggv 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 LAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVALLGFSYR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 targrfatvveelfrdgvnwgrivaffefggvmcvgsvnremsplvdnialwmteylnrh 181
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).

-1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

EMBL: L14680; 6408947; -
APOPTOSIS: ALTERNATIVE SPLICING; TRANSMEMBRANE; MITOCHONDRION.
TRANSMEM. 209 230
-i- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, A PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                  -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; L31532; G387109; -2
EMBL; L31532; G387109; JOINED.
EMBL; R425960; TVMSA1.
PIR; R37332; E3733.
PRS: E37332; E37332.
PROSTUE; PSO1080; BCL2.
TRANSMEM.
209 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                          Length 236
                                                                                                                                                                                                                                                                                                                  Score 251; DB 1; Length 236
Pred. No. 8.18e-26;
31; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.1%; Score 250; DB 1; Length 236 Best Local Similarity 27.2%; Pred. No. 1.25e-25; Matches 40; Conservative 43; Mismatches 60; Indels
                                                                                                                                                                                                                                                209 230 POTENTIAL.
236 AA; 26425 MW; 7ADFE975 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 230 POTENTIAL.
236 AA; 26550 MW; 336E6B40 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 -lhtwiqdnggwdafvel-ygpsmrpl 206
                                                   DIFFER AT THEIR C-TERMINAL ENDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (REL. 34, CREATED)
                                                                                                                                                                                                                                                                                                                     / Match
Local Similarity 30.4%;
nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN BCL-2 ALPHA.
BCL2 OR BCL-2.
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-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELL'A ARE GENERATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.0%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=B-CELL;
MEDLINE; 93364978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 12
BAXB_HUMAN
Q07814;
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 nmelgrmiadvdtdspre-vff-rvaadmfadgnfnwgrvvalfyfasklvlkalctkvp 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: : :|| |: :|| : ::|| 1. ::|| 1. |: |- |: ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|| 1. ::|
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MEDLINE; 93364978.

MEDLINE; 93364978.

CELL 74:609-619(1993).

-1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BCL 2.

-1- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 seqimktgafllqgfiqdragrmagetpeltleqppqdastk-klseclrrigdelds-- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BGL-2.
SUBUNT: FORMS HOWODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
SUBCELLULAR LOCATION: MEMBRANE.
                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 14.2%; Score 221; DB 1; Length 192; Local Similarity 25.6%; Pred. No. 2.37e-20; hes 46; Conservative 50; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                                                                     01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-07-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BD035304 CRC32;
                                                                                                                                            192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 93364978.
OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
CELL 74:609-619(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192
166 CIARWIAQRGGWVAALNLGNGPILNVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                         PRT;
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                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                        LT 10
BAXA_MOUSE
Q07813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAXA_HUMAN
Q07812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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47 QEAEGAAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAEN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 qdragrmggeapelaldpvpqdastkklseclkrigdelds--nmelgrmiaavdtdspr 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 qdragrmggeapelaldpvpqdastkklsec1krigdelds--nmelgrmiaavdtdspr 89
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-:- SUBCELLULAR LOCATION: CYTOPLASMIC.
-:- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
-:- SIMILARTY: BELONGS TO THE BCL-2 FAMILY.
-- FAMILY: L22474; G388168; -- PPIR; B47538; B47538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
CELL 74:609-619(19193).
-!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE
APOPTOSIS REPRESSOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
9
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Pred. No. 3.69e-17;
36; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.4%; Score 208; DB 1; Length 192
Best Local Similarity 24.5%; Pred. No. 4.87e-18;
Matches 40; Conservative 45; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 rllgwiqdqggwdgllsyfgtptwqtvtifvagvltasltiwk 189
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, CYTOPLASMIC ISOFORM BETA.
                                                                                                                                                                                                                                                                                                              PROSITE; PSÓ1080; BCL2.
APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
TRANSMEM 172 192 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSULUBU; DULL.
APOPTOSIS; ALTERNATIVE SPLICING.
APOPTOSIS; ALTERNATIVE SPLICING.
AAA. 24220 MW; 82B2FF09 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                               172 192 POTENTIAL.
192 AA; 21184 MW; B2E6148A CRC32;
ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY EMBL; 122473; 6388166; -.
PIR; A47538; A47538.
MIM; 600040; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 tdsprevffrvaadmfsdgnfnwgrvvalfyfasklvlkalctkvpelirtimgwtldf- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLINE; 9533797.

APPE S.S., MATTEL M.-G., OLSEN B.R.;
APPE S.S., MATTEL M.-G., OLSEN B.R.;
GENOMICS 26:592-594 (1995).

-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

EMBL; J19599; G841238; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KOZOPAS K.M., YANG I., BUCHAN H.L., ZHOU P., CRAIG R.W.;
PROC. NATL. ACAD. SCI. U.S.A. 90:3516-3520(1993).
-!- FUNCTION: INVOLVED IN PROGRAMMING OF DIFFERENTIATION AND CONCOMITANT MAINTENANCE OF VIABILITY BUT NOT OF PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA; MAMMALIA;
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 178; DB 1; Length 143;
Pred. No. 7.38e-13;
31; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 lrerllgwiqdqggwdgllsyfgtptwqtvtifvagvltasltiwk 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APOPTOSIS; ALTERNATIVE SPLICING.
SEQUENCE 143 AA; 15772 MW; 71AA1CBD CRC32;
                                                                                                                                                                                          350 AA
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TISSUE-MYELOID LEUKEMIA CELLS;
MEDLINE; 93234528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
11.5%;
Best Local Similarity 27.4%;
Matches 29; Conservative
147 rllgwiqdqggwvrllk 163
                                                                          166 CIARWIAQRGGWVALN 182
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MCL1_HUMAN
Q07820;
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9
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                                                                                                                                                                                                                                                     28 sapsqacrvlqrvafsvqkeveknlksylddfhvesidtariifnqvmekefedgiinwg 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTERNAL SIGNALS.
-!- INDUCTION: BY GRAULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR AND LPS IN MACROPHAGES.
-!- SUBCELLULAR LOCATION: INTRACELLULAR.
-!- TISSUE SPECIFICITY: EXPRESSED IN HEMOPOIETIC TISSUES, INCLUDING BONE MARROW, SPLEEN AND THYMUS.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; L16462; Q293274; -- PROSITE; PS01080; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIN E.Y., ORLOFSKY A., BERGER M.S., PRYSTOWSKY M.B.;
J. IMMUNOL. 151:1979-1988(1993).
-!- FUNCTION: MAY FUNCTION IN THE RESPONSE OF HEMOPOLETIC CELLS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 rivtifafggvllkklpqeqialdvcaykqvssfvaefimnn-tgewirqnggw 140
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; RODENTIA.
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                                                                                                                Length 350;
                                                                                                        Score 179; DB 6; Length 350
Pred. No. 5.01e-13;
29; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN (A1 PROTEIN)
                                                                                                                                                                                                                                                                                                                           273 fvakhlktingescieplaesitd-vlvrtkrdwlvkgrgw 312
                                                                                                                                                                                                                                                                                                                                                                                 137 RLALHIYQRGLTGFLGQVTRFVVDFMLHHCIARWIAQRGGW 177
227 227 OR A.
330 349 POTENTIAL.
350 AA; 37365 MW; 10194B64 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN 24 33 ALA/PRO-RICH.
SEQUENCE 172 AA; 19914 MW; FFD38D6F CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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STRAIN-CBA/J; TISSUE-BONE MARROW;
MEDLINE; 93346743.
                                                                                                        Query Match
Best Local Similarity 25.7%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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HSAL_MOUSE
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Aug 20 11:05:33 1997; MasPar time 8.89 Seconds 685.993 Million cell updates/sec Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>US-08-320-157-9 (1-211) from US08320157.pep 1554 1 MASCQGPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 211

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir51 Database:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Mean 45.185; Variance 108.828; scale 0.415 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	٠,	1.43e - 241	3.45e-237	1.24e-23	5.03e-23	3.55e-23	3.55e-23	7.14e-23	1.43e-22	4.08e-22	5.77e-22	2.31e-21	2.31e-21	1.30e-20	1.30e-20	1.30e-20	1.30e-20	2.60e-20	5.72e-19	5.02e-16	2.74e-14	1.43e-13
	Description		cdn-2 protein - huma	Bak protein - human	apoptosis requlator	transforming protein	BCL-X protein - rat		transforming protein	apoptosis requlator	bcl-x transmembrane	transforming protein	transforming protein			BCL-X-Long - rat	transforming protein	transforming protein	BCL-2 - rat (fragmen	transforming protein	programmed cell deat	bcl-2-associated pro	bcl-2-associated pro
SUMMARIES	a		S58875	S58873	A47537	B37332	S51761	149056	A37332	B47537	149057	TVHUB1	D37332	TVHUA1	TVMSB1	167431	TVMSA1	E37332	167432	S24390	D47538	A47538	B47538
	DB	ij	13	13	13	9	14	14	ω	13	14	~	9	~	~	14	~	ဖ	14	ø	14	13	13
	Query Match Length		211	211	190	216	233	233	233	233	214	202	206	239	199	233	236	237	236	232	192	192	218
æ	Query		100.0	98.4	17.4	17.2	17.2	17.2	17.1	17.0	16.8	16.7	16.5	16.5	16.2	16.2	16.2	16.2	16.0	15.4	14.2	13.4	13.1
	Score		1554	1529	271	267	268	268	266	264	261	260	256	256	251	251	251	251	249	240	220	208	203
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bax - rat (fragment) gene bc1-2 protein - BAX splice form delt BCL2 bomolog MCL1 - hemopoietic-specific beta-glucosidase - S NR-13 protein - quai cytochrome-coxidase coat protein - straw hexose transport pro hexosine synthase (sugar transport prot nyosin heavy chain-B	Ayoucse transport program glucose transport prot sugar transport prot insulin-like growth fructose-permease II HXT7 protein - yeast hexose transporter H
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                                                                                                                                                                                                                                                                                                                                                                               Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr, P.J.
Nature (1995) 374:736-739
Modulation of apoptosis by the widely distributed Bcl-2
                                                                                                     R.; Flemington
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S58873 *type complete
Bak protein - human
bcl-2 homolog; complete
#formal_name Homo sapiens *common_name man
15.Feb-1996 *sequence_revision 01-Mar-1996 *text_change
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:Y #length 211 #molecular-weight 23409 #checksum 801
                                                             06-Sep-1996
$58873; $58872; $58874
$58873
Chittenden, T.; Harrington, E.A.; O'Connor, R.; Fl
C.; Lutz, R.J.; Evan, G.I.; Guild, B.C.
Næture (1995) 374:733-736
Induction of apoptosis by the Bcl-2 homologue Bak.
                                                                                                                                                      ***status preliminary; nucleic acid sequence not shown **molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 98.4%; Score 1529; DB 13; Length 211; Local Similarity 97.2%; Pred. No. 3.45e-237; nos 205; Conservative 5; Mismatches 1; Indels 0.
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REFERENCE $58872 #authors
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Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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                                                                                                                                                                                                                            gene that functions as a dominant
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BCL-X protein - rat
#formal_name Rattus norvegicus #common_name Norway rat
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FICATION #superfamily bcl transforming protein
*X #length 216 #molecular-weight 23492 #checksum 3596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #checksum 5509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length 190 #molecular-weight 21467
                                                                                                                                                cell (1993) 74:597-608
bcl-x, a bcl-2-related gene that fur
regulator of apoptotic cell death.
                                                                                                                                                                                                                                                                                                                                                                                  ##status
preliminary
##molecule_type DNA
##residues 1-190 ##label BOI
##cross-references GB:L20120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
#journal J. Immunol. (1994) 155:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in and T lymphocytes.
#cross-references MUID:95052604
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submitted to the EMBL Data Library, November 1994
IL-5 inhibits anti-IgM-induced apoptosis in an immature
cell line through inductin of bcl-X1.
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#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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#length 233 #molecular-weight 26130 #checksum 6378
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Michaelldis, T.M.
submitted to the EMBL Data Library, November 1994
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##residues 1-233 ##label RES
##cross-references EMBL:U10101; NID:9506647; CDS_PID:9506648
NACE S52866
                                                                                       EMBL Data Library, November 1994
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Pred. No. 3.55e-23;
37; Mismatches 46; Indels
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Pred. No. 3.55e-23;
37; Mismatches 46; Indels
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##cross-references EMBL:X83574
Y #length 233 #molecular-weight 26132
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##cross-references EMBL:X82537
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                                                                Michaelidis, T.M. submitted to the
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Best Local Similarity 28.0%;
Matches 33; Conservative
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Best Local Similarity 28.0%;
Matches 33; Conservative
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S51761; S51762
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##residues 1-2
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Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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                                                                                                                                                                                                                                                       Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
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Dol-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.
                                                                                 transforming protein (bcl-2-alpha) - chicken transforming protein (bcl-2-alpha) - chicken #formal_name Gallus gallus #common_name chicken 03-mar-1993 #sequence_revision 03-mar-1993 #text_change A37332; S35453
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                      nucleic acid sequence not shown; translated from
143 ffsfggalcvesvdkemqvlvsriaswmatylndh-lepwiqenggwdtfvdlygnna
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Pred. No. 7.14e-23;
42; Mismatches 56; Indels
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apoptosis regulator bcl-xS
#formal_name Homo sapiens #common_name man
16-Aug-1996 #sequence_revision 16-Aug-1996
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transforming protein
#length 233 #molecular-weight 25687
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apoptosis regulator bcl-xL - human
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##cross-references GB:L20121; CDS_PID:Q07817
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##cross-references EMBL:D11381
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B47537; C47537
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Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
Analysis of the structure, transcripts, and protein products
of bcl-2, the gene involved in human follicular lymphoma.
                                                                                                                                     #label MAT\
#product apoptosis regulator bcl-xS #status predicted #label MA2
                                                                                                                     *product apoptosis regulator bcl-xL *status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fauthors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.

*Journal J. Immunol. (1994) 153:4388-4398

*title Cloning and molecular characterization of mouse bcl-x in and T lymphosytes.

*cross-references MUID:95052604
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                                                                                                                                                                                                                                                           Gaps
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bcl-x transmembrane deleted - mouse
*formal_name Mus musculus *common_name house mouse
02-Jul-1996 *sequence_revision 02-Jul-1996 *text_change
02-Jul-1996
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#length 214 #molecular-weight 23900 #checksum 9730
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Pred. No. 4.08e-22;
33; Mismatches 43; Indels
                                                                                                                                                                                                                    Score 264; DB 13; Length 233; Pred. No. 1.43e-22;
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                                                                                                                                                                                                                                                         37; Mismatches 46; Indels
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##rosidues 1-69,'G',71-125,189-233 ##label BO2
##cross-references GB:L20122; CDS_PID:g623237
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##cross-references GDB:228079
alternative splicing; apoptosis
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Best Local Similarity 28.0%;
Matches 33; Conservative
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Best Local Similarity 28.0%;
Matches 30; Conservative
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#gene GDB:BCL2
##cross-references GDB:119031
#map_position 18q21.33-18q21.33
CLASSIFICATION #superfamily bcl transforming protein
Alternative splicing; B-cell lymphoma; follicular lymphoma;
transforming protein
SUMMARY #length 205 #molecular-weight 22182 #checksum 1183
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Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
                                                                                                                                                                                                                                                                                                                                                                                                                                  132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
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Pred. No. 5.77e-22;
37; Mismatches 49; Indels
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*length 206 *molecular-weight 22440
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Pred. No. 2.31e-21;
35; Mismatches 51;
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#accession bd>ywv.
##molecule_type mRNA
##molecule_type mRNA
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Best Local Similarity 29.7%;
Matches 38; Conservative
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Best Local Similarity 29.7%;
Matches 38; Conservative
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1-233 ##label RES
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##residues 1-23
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#journal Exmbo J. (1988) 7:123-131
#fitle Alternative promoters and exons, somatic mutation and derequiation of the Bcl-2--Ig fusion gene in lymphoma.
#cross_references_MUID:88196071
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Nucleic Acids Res. (1992) 20:4187-4192
Sisolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
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alternative splicing: B-cell lymphoma;
proto-oncogene; transforming protein
#length 239 #molecular-weight 26266 #checksum 8323
                                                                                                                                                                                                                                                                                                                                                        1-95,'A',97-109,'G',111-236,'S',238-239 ##label TSU
this sequence has been corrected in reference A37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                idues 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 ##label HUA2 the sequence was determined from the germline gene Constitutive expression of BCL2 following t(14:18) chromosomal translocation is typically found in follicular lymphoma.
                                                                                                                                          nucleic acid sequence not shown; not compared with conceptual translation
               C37332; A29409; S02452; A24428; A27622; B27622
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##molecule_type mRNA
**residues 1-58,'T',60-116,'R',118-239 ##label
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                                                                                                                                                                                      1-239 ##label EGU
this report is a correction
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##residues 1-58,'T',60-239 ##label HUA
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##residues 1-239 ##label SET
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#map_position 18q21.33-18q21.33
06-Sep-1996
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##molecule_type mRNA
##residues 1-95,
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##residues 1-6,
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##residues 1-23
##note this
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                                                                                                                                            ##status
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                                                                #journal
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               ACCESSIONS
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Cell (1987) 49.455-463
Molecular analysis of mbcl-2: structure and expression of the
murine gene homologous to the human gene involved in
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#journal Endocrinology (1995) 136:232-241
#title Expression of members of the bol-2 gene family in the Immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bol-2 and bol-xlong messenger ribonucleic acid levels.
#cross-references MUID:95129487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                        74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargrfa 131
                                                                                                                                  132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 LAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVALLGFSYR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transforming protein bol-2-beta - mouse
#formal_name Mus musculus #common_name house mouse
31-bec-1988 #sequence_revision 31-bec-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCL-X-Long - rat
#formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
26-Jul-1996
167431
                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily bcl transforming protein
alternative splicing; transforming protein
#length 199 #molecular-weight 22299 #checksum 7397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 251; DB 2; Length 199;
Pred. No. 1.30e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Mismatches 41; Indels
Best Local Similarity 29.3%; Pred. No. 2.31e-21; Matches 41; Conservative 37; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwvga 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #type complete
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cross-references MUID:87187643
                                                                                                                                                                                                                                                                                                                                                           : ||| | ::| || : |
173 QRGGWVAALNLGNGFILNVL 192
                                                                                                                                                                                                                                                                                                                         191 dnggwdafvel-ygpsmrpl 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.2%;
Best Local Similarity 31.1%;
Matches 32; Conservative
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B25960
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                                                                                                                        83 maavkqalreagdefelryrrafsdltsqlhitpgtvyqsfeqvvnelfrdgvnwgriva 142
                                                                                                                                                           71 MGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
                                                                                                                                                                                                                                                                                                      Score 251; DB 14; Length 233;
Pred. No. 1.30e-20;
34; Mismatches 48; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              #journal Cell (1987) 49:455-463
#title Molecular analysis of mbcl-2: structure and expression murine gene homologous to the human gene involved in follicular lymphoma.
#cross-references MUID:87187643
#accession A25960
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                                                                                                                                                                                            BCL2
192/3
#superfamily bcl transforming protein
#ternative splicing; transforming protein
#length 236 #molecular-weight 26524 #checksum 6709
##cross-references EMBL:034963; NID:91004376; CDS_PID:91004377 (Y #length 233 #molecular-weight 26122 #checksum 8310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
16.2%; Score 251; DB 2; Length 236; Best Local Similarity 30.4%; Pred. No. 1.30e-20; Matches 35; Conservative 31; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
##rmsidues 1-236 ##label NEG
                                                 Query Match
Best Local Similarity 27.6%;
Matches 32; Conservative
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Aug 20 11:08:18 1997; MasPar time 3.38 Seconds 298.086 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-21 (1-88) from US08320157.pep 643 Title: Description: Perfect Score: Sequence:

1 MASGQGPGPPRQECGKPALP.....APWGRWDGSSPSPGRHQPAL 88

PAM 150 Gap 11 Scoring table:

96640 seqs, 11439865 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 a-geneseq27 Database:

Variance 105.074; scale 0.264 Mean 27.717; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.98e-58	3.66e-12	3.66e-12	3.66e-12	3.66e-12	3.66e-12	7.53e+00	9.13e+00	1.11e+01	1.34e+01	1.34e + 01	1.34e+01	1.62e+01	1.62e+01	1.62e+01	1.95e+01	2.36e+01	2.36e+01	3.43e+01	3.43e+01
Description	Human Cdn-3.	Bak-2 protein.	Human Cdn-1.	Bak protein.	Bcl-Y apoptosis-relat	Human Cdn-2.	Xenopus laevis HSP (x	Mature mouse sperm 70	Gallus gallus HSP (ch	Human interleukin-I-c	Aromatic dihydrodiol/	Human neuronal calciu	HSV L/ST ORF1.	Murine Natural Killer	Partial Human Natural	Mouse SLIP1 homologue	MN protein.	Rat HSP (rathsp70).	Human alpha-1A adrene	Human alpha-1A adrene
ឧ	R77878	W03669	R77876	W03668	R81451	R77877	R03928	R43004	R03930	R95830	R66729	R71007	R64327	R13320	R13319	R43002	R41746	R03927	R70996	R90040
DB	13	20	13	20	17	13	'n	œ	Ŋ	18	13	14	13	ო	m	œ	œ	S	12	18
Suery Match Length	88	211	211	211	211	211	647	641	634	341	459	2510	233	982	1023	633	429	646	501	501
Ouery Match	100.0	33.1	33.1	33.1	33.1	33.1	13.1	12.9	12.8	12.6	12.6	12.6	12.4	12.4	12.4	12.3	12.1	12.1	11.8	11.8
Score	643	213	213	213	213	213	84	83	82	81	81	81	80	80	80	79	78	78	92	92
Result No.	П	7	m	4	S	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20

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61 spcpsnlaapwgrwdgsspspgrhqpal 88 SPCPSNLAAPWGRWDGSSPSPGRHQPAL 88

61

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3.43e+01 4.966e+01
Insulinoma-associated erya region polypepti Phytase protein. BRCAI mutant from pat BRCAI allele #977 tran BRCAI allele #8403 tr BRCAI mutant from PM2 BRCAI mutant from PM2 BRCAI mutant from PM2 BRCAI mutant from PM0 BRCAI mutant from Sam BRCAI mutant from pat
R34674 R844430 R818619 R818619 R99448 R99440 R99440 R81542 R81535 R81535 R81533 R81533 R81533 R81533 R81533 R81539 R81519 R81519 R81519 R81519 R81519 R81519 R81519 R81519 R81519 R81519 R81519 R81518
8 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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ALIGNMENTS

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New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                 Cdn-3; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig.7B-C; 66pp; English.

Southern blot analysis of human genomic DNA and a panel of human/rodent somatic cell DNAs revealed at least 3 Cdn-related genes residing on chromosomes 6, 11 and 20. Cdn-3 (R77878) and an octon the structural features of Cdn-1 (R77876), Cdn-2 (R77877) or othat Bcl-2 family members.
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Pred. No. 1.98e-58;
0; Mismatches 0; Indels
    T
R77878 standard; Protein; 88 AA.
                                                                                                                            Homo sapina.

W09515084-A.

W09515084-A.

W09515084-A.

30-NOV-1994; U13930.

30-NOV-1994; US-160067.

07-OCT-1994; US-320157.

(LKRB-) LXR BLOTECHNOLOGY INC.

BALT PJ. Kiefer MC;

WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 88; Conservative
                                                21-NOV-1995 (first entry)
                                                                  Human Cdn-3
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WO9633416-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Bak-2 protein sequence represents a bol-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak-2 and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; 095492.
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
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Cdn-1 cDNA was isolated from a human heart cDNA library using a Cdn-1 cDNA was isolated from a human heart cDNA library using a proviously isolated clone as probe. Recombinant Cdn-1 was produced in $f9 and human colon adenocarcinoma HT29 calls. Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
                                                                                                                                      Human; Bak-2; apoptosis; latency; virus replication;
Bpstein-Barr virus; BHRF1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
protein interactive trapping; virucide; antitumour; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 33.1%; Score 213; DB 20; Length 211; Local Similarity 78.0%; Pred. No. 3.66e-12; Os 32; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 masgqgppprqecgepalpsaseeqvaqdteevfrsyvfy 41
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W03669 standard; Protein; 211 AA W03669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
Disclosure; Fig 2; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R77876 standard; Protein; 211 AA.
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30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB.) LXR BIOTECHNOLOGY INC.
Barr PJ, K10fer MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                  24-OCT-1996.
19-APR-1996.
20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY INC.
BART PJ. Klafer MC;
WPI; 96-485866/48.
N-PSDB; T42139.
                                                                     22-FEB-1997 (first entry)
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Sequence 211 AA;
                                                                                                         Bak-2 protein.
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                                                                                                                                                                                                                                                                                    Homo saptens
WO9633416-Al
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This Bak protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compounds which
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                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                     Human; Bak; apoptosis; latency; virus replication; Epstein-Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; immunoassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-Y apoptosis-related protein.
Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 211;
  Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 213; DB 20; Length 21
Pred. No. 3.66e-12;
2; Mismatches 6; Indels
                                                    Indels
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9
                                                                                                      1 masgqqppprqecgepalpsaseeqvaqdteevfrsyvfy 41
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/note= "putative membrane localisation sequence"
22-per-14.
Score 213; DB 13;
Pred. No. 3.66e-12;
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
188..205
                                                                                                                                                                                                                                                              W03668 standard; Protein; 211 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-1996; U05639.
20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY INC.
Balt PJ, Klefer MC;
WPI; 96-485886/48.
33.1%;
78.0%;
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78.0%;
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                                                                                                                                                                                                                                                                                                                   22-FEB-1997 (first entry)
                        Best Local Similarity 78.0%;
Matches 32; Conservative
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09-AUG-1995; U10103.
09-AUG-1994; US-287427.
11-OCT-1994; US-321071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 32; Conserv
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Query Match
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                                          New isolated human Bcl-Y protein - used to develop prods, for treating disorders characterised by inappropriate cell proliferation or cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q95493.
New nucleic acid sequences encoding Cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                             Claim 3; Fig 4; 100pp; English.

BC1-Y protein (R81451) is a member of the BC1-2 family and can induce apoptosis in cells and function as a negative regulator of BC1-2 function.

BC1-2 function.

BC1-2 function.

BC1-2 function.

BC1-2 function.

BC1-2 function all human tumour cell lines examined and is also widely expressed in primary human tissues. It can be obtd. by expression of a full-lingth connocione (T17375) in pref. mammalian host cells.

BC1-Y can be used to develop prods. for treating disorders associated with inappropriate cell proliferation or cell death, and to raise antibodies used for sequence 211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  etc.
Disclosure; Fig.5D-E; 66pp; English.
Cdn-2 cDNA was isold. from a human placental genomic library using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein displayed 97% amino acid identity with Cdn-1 (R77876).
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R03928;
30-40G-1990 (first entry)
Xenopus laevis HSP (x170).
HSp70; heat shock protein; Trypanosoma cruz1; vaccines; HSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 213; DB 17;
Pred. No. 3.66e-12;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 213; DB 13;
Pred. No. 3.66e-12;
2; Mismatches 6
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30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LARB-) LAR BIOTECHNOLOGY INC.
BARY PJ, KLOFER MC;
WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 6
R77877 standard; Protein; 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.1%;
Best Local Similarity 78.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.1%;
Best Local Similarity 78.0%;
Matches 32; Conservative
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                        WPI; 96-139648/14.
N-PSDB; T17375.
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WO9515084-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R77877;
21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Cdn-2
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ID RO
AC RO
DT 30
DE Xe
KW HE
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                                                                                                                                                                                                                             in vaccines and diagnosis for species of eg Mycoplasma ornuzi-used in vaccines and diagnosis for species of eg Mycoplasma or Mycobacteria. Disclosure; Fig 2.1-2.14; 86pp; English.

Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.Hyopneumoniae (Mhyhsp70 - R03922);
2. Bacillus megaterium (Bmehsp70 - R03923);
3. E. coli (dnaK - R03924);
4. T. cruzi (R03926);
5. T. cruzi (R03926);
6. Rat rattus (rathsp70 - R03927);
7. Xenopus laevis (x170 - R03928);
8. Homo sapiens (humhsp70 - R03929);
9. Gallus gallus (chkhsp70 - R03930);
10. Zea mays (mzehsp70 - R03931);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                           Proteins homologous to heat shock proteins from Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11. Serratia marcescens (smahspio - R03932).
The proteins having homology to hsp's of T. cruzi can be used in accines and diagnosis involving e.g. Trypanosoma, Mycoplasma and Mycobacteria species.
Sequence 647 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MX-1994 (first entry)
Mature mouse sperm 70kD heat shock protein.
Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
HSC70B; mammalian; infertility; mycoplasma; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
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Pred. No. 7.53e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 rtacdrakrtlssssqasieidslfegidfytaitrar 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the peptides are homologous to sequences conserved between SLIP1 and 74.5kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8

R43004 standard; protein; 641 AA.

DE R43004

T 20-MAY-1994 (first entry)

DE Mature mouse sperm 70kD heat shock p

KW Sulphoglycolipid immobilising protein

KW MISC70B; mammalian; infertility; mycc

Mus musculus.

Location/Qualifiers

FT Kegion

FT /label= 44kD_ATPase_fragment

FT /label= 44kD_ATPase_fragment

FT /note= "peptides comprissing an intac

FT /note= "peptides are homologous to seque

FT mycoplasma protein.

FT /note= "part"

FT /note= 
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12-SEP-1989; 03955.
12-SEP-1988; US-243474.
(CODO-) COGON.
Dragon E, Faulds D, Sias S.
WPI: 90-115820/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 26.3%;
Matches 10; Conservative
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US-08-320-157-21.rag

Matches

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Human interleukin-I-converting enzyme-like apoptosis protease-3. 
ICE-LAP-3; interleukin-I-converting enzyme-like apoptosis protease; enzyme; Alzheimer's disease; Parkinson's disease; septic shock; head injury; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Numan ICE-LAP-3 and -4 DNA and protein - useful in the diagnosis and treatment of Alzheimer's disease, Parkinson's disease, rheumatoid arthritis, septic shock and head injury claim i, Page 91-92; 67pp; English.

This ICE-LAP-3 protein may be used therapeutically, e.g. as an antitumor or antiviral agent and to control embryonic development and tissue homeostasis. The protein can also be used to treat immunosuppression disorders, such as AIDS, by targeting virus infected cells for cell death. The DNA may find use in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.6%; Score 81; DB 18; Length 341; Best Local Similarity 40.0%; Pred. No. 1.34e+01; Matches 12; Conservative 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                     06-JUN-1995; U07235.
01-NOV-1994; US-334251.
(HUMA-) HUMAN GENOME SCI INC.
Hastings GA, He W, Hudson PL, Rosen CA;
WPI; 96-239509/24.
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                                                           R95830 standard; Protein; 341 AA. R95830;
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R66729 standard; Protein; 459
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ilarity 30.0%;
Conservative
                                                                                                              (first entry)
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10-JUN-1993; 165163.
10-JUN-1993; JP-165163.
(SHOW ) SHOWA DENKO KK.
WPI; 95-069306/10.
N-PSDB; Q79907.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T15276
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                                                                                                                 28-OCT-1996
                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                     09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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WITH VALIDS AND AUGOGUUS to heat shock proteins from Trypanosoma cruzi - used no vaccines and diagnosis for species of eq Mycoplasma or Mycobacteria. Fig 21-21-214; 86pp; English.

Discloaure; Fig 2.1-2.14; 86pp; English.

According to the legend of Fig 2, the G gallus HSP sequence has 535 amino acid residues, the sequence itself has only 634,

Including "O" (?) at position 634.

Including "O" (?) at position 634.

C fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - R03922);

C 2. Bacillus megaterium (Bmehsp70 - R03923);

C 3. E. coli (dnaK - R03924);

C 4. T. cruzi (R03926);

C 5. T. cruzi (R03926);

C 6. Rat rattus (rathsp70 - R03929);

C 7. Xenopus laevis (x170 - R03929);

C 8. Homo sapiens (humhsp70 - R03929);

C 10. Zea mays (mzehsp70 - R03932);

C 11. Serratia marcescens (smahsp70 - R03932);

C 12. Serratia marcescens (smahsp70 - R03932);

C 13. Serratia marcescens (smahsp70 - R03932);

C 2. Vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and contents and
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                                                                                                                                                                                 The likelihood of mammalian fertilisation is decreased by contacting a gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated glyco-molety interfering composition. The interfering composition. The interfering composition. The interfering such as the mouse SLIP1 analogue "HSC70B" comprising the amino acid sequence R43002) or the 74.5kD mycoplasma protein (R43003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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(OTTA-) OTTAWA CIVIC HOSPITAL.

Faulds DH, Lingwood CA, Tanphaichitr N;
WPI; 93-36422/46.

Mammalian fertilisation decrease for detecting and treating infertility - using sulpho glyco lipid immobilising protein linfertility - using sulpho glyco lipid immobilising protein l-sulphated-glyco molety interfering compsn., for mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-1990 (first entry)
Gallus gallus HSP (chkhsp70).
H8p70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82; DB 5; Length 634;
Pred. No. 1.11e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 12.9%; Score 83; DB 8; Length 641; Local Similarity 26.3%; Pred. No. 9.13e+00; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 rtacerarrtlssstqasieidslfegidfytsitrar 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 rtacerakrtlssstgasleidslfegidfytsitrar 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | :: :| | : ::: | | RQECGKPALPSASEEQVAQDMEG-FSAATFFTTISRNR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "residue given as "O" in specification" W09002564-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R03930 standard; Protein; 634 AA.
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26.3%;
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WPI; 90-115820/15.
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12-SEP-1988; US-243474.
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                                                                                                                                                                                                                                                                                                                                                                           641 AA;
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Misc_difference
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Matches
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Gaps

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protein sequences (Talm 1) Page 8-9; 13pp; Japanese.

The enzymes (R66729-34), encoded by genes 079907-12, are involved in the synthesis of dihydrodiol and catechol compounds by microbial fermentation in E.coll at normal temps. and pressures from aromatic Phydrocarbons.

The sequence presented here its of an aromatic deoxygenase of 459 amino acids. The aromatic dihydrodiol can be used as a raw material for engineering plastics and the catechol compound is used as a polymerisation inhibitor of synthetic resin and as an intermediate in drug synthesis.
02-0CT-1995 (first entry)
Aromatic dihydrodiol/catechol deoxygenase #1.
Dihydrodiol; catechol; microbial fermentation; E.coli; aromatic;
deoxygenase; hydrocarbon; engineering plastic; polymerisation inhibitor;
synthetic resin; drug synthesis.
Pseudomonas fluorescens SD805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prepn of an aromatic cyclic di:hydro:diol opd and a catechol using microbial cells transformed by DNA coding for enzyme
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Pred. No. 1.34e+01;
13; Mismatches 26; Indels
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                             developing prods. for studying calcium channels, e.g. for obtaining agonists and antagonists.

The primary prods. for studying calcium channels, e.g. for obtaining agonists and antagonists.

Claim 34: Page 178-190; 285pp; English.

The primary transcelpt of the alpha 1A subunit gene is alternatively spliced to yield at least two variant mRNAS.

One form, alpha 1A-1 is given in Q84659/R71008. Alpha 1A-2 differs from alpha 1A-1 is given in Q84659/R71008. Alpha 1A-2 differs from alpha 1A-1 encoding sequence at the 3' end in that it lacks a first sequence. This deletion shifts the reading frame and introduces a translation termination codon resulting in an alpha 1A-2 coding sequence that encodes a shorter alpha 1A subunit than that encoded by alpha 1A-1. DNA doncding alpha 1A subunit than that encoded by alpha 1A-1. DNA doncding alpha having sequence Q84661, Q85559 or Q84660 or DNA encoding an alpha the phage lysate of an E. coll host contg. DNA encoding an alpha 1A-2 bunit that has been deposited in the ATCC under accession no. 75293. The DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of the DNA is such a phage includes the DNA fragment of th
Gaps
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N-PSDB; 076209.
N-PSDB; 076209.
- for inhibiting HSV L/ST synthesis, in the treatment of HSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                               16-FEB-1995.
11-ANG-1994 UO9230.
11-ANG-1993; US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME; 95-090900/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81; DB 14; Length 2510;
Pred. No. 1.34e+01;
12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSV; junction spanning transcript; L/ST; therapy; virucide. Herpes simplex virus type 1. WO9428156-A.
                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                              01-DEC-1995 (first entry)
Human neuronal calcium channel subunit alpha 1A-1.
Calcium channel subunit; antagonist; agonist; diagnosis;
Lambert Eaton Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2235 agerpdhgrarardgrwsrspsegrehmahrggsssvsgspaps 2278
                                                                                                                                                                                                                                                                                                                                                                   DNA encoding human calcium channel sub-unit(s) - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 SRNRRLKGRPPLPTORWSPCPSNLAAPWGRWDGSSPSPGRHQPA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 34-35; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1994.
20-MAY-1994; U05770.
20-MAY-1993; US-065146.
CDAND ) DANA FARBER CANCER INST INC.
Schaffer PA, Yeh L;
                                                                                   T 12
R71007 standard; Protein; 2510 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R64327 standard; Protein; 233 AA
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Best Local Similarity 31.8%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding alpha 1B
quence 2510 AA;
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                                                                                                                                                                                                  Homo sapiens.
WO9504822-A.
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Overlapping clones, which make up the cDNA sequence from which this sequence was deduced, were isolated from a murine PBL cDNA library prepared in lambda gt10. The purified protein can mediate the cytolytic activity of mammalian cells. It specifically distinguishes tumour cells making it a candidate for the development of products for the immunodetection and immunotherapy of tumours.
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
In HSV-1, 4 intron-less open reading frames (ORFS) are present within the sequence specifying the L/ST junction-spanning transcript. ORPI-4 are given in Q76209-12, and encoded proteins in R64327-30. Antibodies raised against such proteins may be used to identify therapeutic agents. Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a natural killer cell receptor - used to develop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding a natural killer cell receptor - used to develop prods. for the immuno-detection and immuno-therapy of tumours
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                                                                                                                                                                        Length 233;
                                                                                                                                                                                                                      14; Indels
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6
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Pred. No. 1.62e+01;
12; Mismatches 14;
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Partial Human Natural Killer receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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R13319 standard; Protein; 1023 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine Natural Killer receptor. NK; cytotoxic drugs; tumour cell.
                                                                                                                                                                                                                                                                                                                                                                                  n 14
R13320 standard; Protein; 982 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NK; cytotoxic drugs; tumour cell Homo sapiens.
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08-JUN-1990; 08-535206.
(USSH) NMT INST OF HEALTH.
Ortaldo J, Young H, Anderson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= partial_signal_peptide US7535206-A.
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Ortaldo J, Young H, Anderson
WPI; 91-245694/33.
N-PSDB; Q13114.
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Best Local Similarity 38.2%;
Matches 13; Conservative
                                                                                                                                                                 Query Match 12.4%;
Best Local Similarity 32.5%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein 8.982
/label= mature_NK_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1991 (first entry)
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08-JUN-1990; 143578.
08-JUN-1990; US-535206.
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N-PSDB; Q13115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo saplens.
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prods. for the immuno-detection and immuno-therapy of tumours Disclosure; Fig 1; 30pp; English.
Overlapping clones, which make up the cDNA sequence from which this sequence was deduced, were isolated from a cDNA library prepared from human NK calls purified from human peripheral blood. The purified protein can mediate the cytolytic activity of mammalian calls. It specifically distinguishes tumour cells making it a candidate for the development of products for the immunodetection and immunotherapy of tumours. See also Q13115.
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	Gaps
	4,
jth 1023;	Indels
L;	œ ;
Score 80; DB 3; Length Pred. No. 1.62e+01;	9; Mismatches 8;
12.4%;	vative
nilarity	Conser
h Str	13
Query Match Best Local Similarity 38.28	Matches

⁴¹⁰ qrlrayrpp-sgekwsk-gdklsdpcssrwders 441 :||| :||| | :||| | 47 RRLKG-RPPLPTQRWSPCPSNLAAP-WGRWDGSS 78 à

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Search completed: Wed Aug 20 11:08:43 1997 Job time : 25 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Aug 20 11:09:01 1997; MasPar time 5.05 Seconds 503.601 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-21 (1-88) from USO8320157.pep 643 1 MASGQGPGPPRQECGKPALP......APWGRWDGSSPSPGRHQPAL 88 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

91006 segs, 28888923 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Mean 37.327; Variance 80.459; scale 0.464 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	9.18e-20	9.18e-20	1.35e-01	7.82e-01	1.84e+00	2.43e+00	2.43e+00	3.21e+00	3.21e+00	3.21e+00	3.21e+00	3.21e+00	3.21e+00	3.21e+00	3.21e+00	3.21e+00	4.23e+00	4.23e+00	4.23e+00	4.23e+00	4.23e+00
	Description	cdn-2 protein - huma	Bak protein - human	heat shock protein Y	Shb protein - human	heat shock protein 7	globulin 1 - eastern	heat shock coquate p	70k heat shock coqua	heat shock protein S	heat shock cognate p	heat shock protein S	shock	heat shock protein 7	heat shock protein 7	genome polyprotein -	MHC class III histoc	heat shock protein 7	copy control protein	regulatory protein G	alpha-L-fucosidase (heat shock protein 7
SUMMARIES	ΩI	S58875	S58873	A40623	S37577	20603	S18156	A36333	A48872	S20139	S37394	HHBYA1	S25585	HHXL70	S18349	S26369	B35098	B44261	B47092	JC1495	S10235	S31766
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Nature (1995) 374:736-739
Modulation of apoptosis by the widely distributed Bci-2
homologue Bak.
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K.T.; Grinham, C.J.; Martinou, J.C.; Brown, R.
Nature (1995) 374.731-731.
Cloning of a bcl-2 homologue by interaction with adenovirus
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heat shock protein Y - Escherichia coli
*formal_name Escherichia coli
21-Sep-1993 *sequence_revision 18-Nov-1994 *text_change
15-Nov-1996
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Missiakas, D.; Georgopoulos, C.; Raina, S.
Missiakas, D.; Georgopoulos, C.; Raina, S.
The Bacterioli (1993) 175:2613-2624
The Escherichia coli heat shock gene htpY: mutational analysis, cloning, sequencing, and transcriptional
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DNA Seq. (1993) 3:327-332
Five open reading frames upstream of the dnaK gene of
Escherichia coli.
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##cross-references GDB:635887
:Y #length 211 #molecular-weight 23409 #checksum 801
##molecule_type mRNA
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##cross-references NCBIN:130422; NCBIP:130423
##note sequence extracted from NCBI backbone
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Best Local Similarity 78.0%; Pred. No. 9.18e-20;
Matches 32; Conservative 2; Mismatches 6;
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##cross-references EMBL:X84213
REPERENCE $58874
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The human heat-shock protein family. Expression of a novel heat-inducible HSP70 (HSP70B') and isolation of its cDNA and genomic DNA.
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Shb protein - human
#formal_name Homo sapiens *common_name man
06-Jan-1995 *sequence_revision 06-Jan-1995 *text_change
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heat shock protein 708' - human
*formal_name Homo sapiens #common_name man
30.Sep-1991 *sequence_revision 30-Sep-1991 *text_change
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heat shock; stress-induced protein
#length 196 #molecular-weight 21225 #checksum 5329
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Y #length 596 #molecular-weight 64525 #checksum 5363
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#map_position 1cen-1qter
CLASSIFICATION #superfamily heat shock protein 70
SUMMARY #length 643 #molecular-weight 70853 #checksum 313
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submitted to the EMBL Data Library, October 1993
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                                                                                              Score 95; DB 9; Length 196;
Pred. No. 1.35e-01;
2; Mismatches 7; Indels
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**residues 1-643 **label LEU
**cross-references EMBL:X51757
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#accession S09036
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Best Local Similarity 57.1%;
Matches 12; Conservative
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##residues 1-59
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J. Biol. Chem. (1993) 268:23267-23274
Aginactin, an agonist-regulated F-actin capping activity is
                                 globulin 1 - dattern white pine

#formal_name Pinus strobus #common_name eastern white pine

6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change

06-Jan-1995
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Perrimon, N.; Craig, E.A.
#journal Mol. Cell. Biol. (1990) 10:3232-3238
#title Molecular and developmental characterization of the heat shock cognate 4 gene of Drosophila melanogaster.
#cross-references MUID:90258915
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70k heat shock cognate protein aginactin - slime mold
(Dictyostelium discoideum) (fragment)
F-actin capping protein aginactin
#formal_name Dictyostelium discoideum
19-May-1995 #sequence_revision 19-May-1995 #text_change
03-May-1996
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25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change
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heat shock cognate protein 70 - fruit fly (Drosophila
melanogaster)
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##cross-references EMBL:211486
Y #length 488 #molecular-weight 54715 #checksum 3250
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#length 651 #molecular-weight 71059 #checksum 805
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                                                                                                                                        Rugh, C.L.; Kamalay, J.C.
submitted to the EMBL Data Library, November 1991
                                                                                                                                                                                                                                                                                                                                Length 488;
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13.2%; Score 85; DB 7; Length 651;
Best Local Similarity 26.3%; Pred. No. 2.43e+00;
Matches 10; Conservative 13; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                            Score 85; DB 10; Length 488
Pred. No. 2.43e+00;
7; Mismatches 14; Indels
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Best Local Similarity 36.1%;
Matches 13; Conservative
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Purnelle, B.; Goffeau, A. submitted to the EMBL Data Library, April 1996
The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14 open reading frames among which HSP104, SSA2, SPA2, KNSI, DPS1/APS, SDC25, a new member of the seripauperins family and a new ABC transporter homologous to the human multidrug resistance protein.
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residue 350 as Thr,
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submitted to the Protein Sequence Database, May 1996
S64772
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Nucleic Acids Res. (1989) 17:805-806
The SSAl and SSA2 genes of the yeast Saccharomyces
cerevisiae.
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associated with an Hsc70 in Dictyostelium.
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S20139; S64772; S64775; S69383
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##rosidues 72-639 ##label DUE
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##experimental_source strain S288C
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##cross-references EMBL:X12927
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##molecule_type DNA
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##residues 1-6:
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Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.;
Zeng, B.; Delaney, S.; Ouellette, B.F.; Barton, A.B.;
Kaback, D.B.; Bussey, H.
Yeast (1994) 10:535-541
Sequencing of chromosome I of Saccharomyces cerevisiae:
analysis of the 42 kbp SPO7-CENI-CDC15 region.
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heat shock protein SSA1 - yeast (Saccharomyces cerevisiae)
heat shock protein 70-related protein SSA1; heat shock
protein YG100; protein YAL005c
#formal_name Saccharomyces cerevisiae
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                Haus, U.; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Schleicher, M. EMBO J. (1993) 12:3763-3771 The heat shock cognate protein from Dictyostellum affects actin polymerization through interaction with the actin-binding protein cap32/34.
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heat shock cognate protein 70 - slime mold (Dictyostelium
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31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
12-Apr-1995
 molecular chaperone
#length 639 #molecular-weight 69469 #checksum 5309
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*length 640 *molecular-weight 70499 *checksum 4857
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                                                    Score 84; DB 7; Length 639;
Pred. No. 3.21e+00;
12; Mismatches 15; Indels
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Pred. No. 3.21e+00;
12; Mismatches 15; Indels
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##note the nucleotide sequence was submitted
Library, November 1993
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**cross-references EMBL:X75263
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Best Local Similarity 26.3%;
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Dezeure, F.; Vaiman, M.; Chardon, P.
Blochim. Biophys. Acta (1993) 1174:17-26
Characterization of a polymorphic heat shock protein 70 gene
in swine outside the SLA major histocompatibility complex.
$34625
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heat shock protein 70 - pig
#formal_name Sus scrofa domestica *common_name domestic pig
20.Feb-1995 *sequence_revision 20-Feb-1995 *text_change
03-Aug-1995
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submitted to the EMBL Data Library, June 1993
S42164
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13.1%; Score 84; DB 3; Length 642;
Best Local Similarity 26.3%; Pred. No. 3.21e+00;
Matches 10; Conservative 12; Mismatches 15; Indels
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##molecule_type DNA
##residues 1-642 ##label SLA
                                                                                                                             ##cross-references EMBL:X12926
                                                                                                                                                                                                                                                                                                                                                                                                               LISTA:SSA1; YG100
#cross-references MUID:89128457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A03310; A22175
A90993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S34625; S25585
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                       S25438
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S26369

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Search completed: Wed Aug 20 11:09:37 1997 Job time: 36 secs.
         #accession
                                                                                                                                           KEYWORDS
FEATURE
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                                                                                                                                                                                                                                                                                                                               SUMMARY
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EMBO J. (1984) 3:2477-2483
Xenopus hsp 70 genes are constitutively expressed in injected
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                                                                                                                                                                   #authors Bienz, M. #500 Sci. U.S.A. (1984) 81:3138-3142 Proc. Natl. Acad. Sci. U.S.A. (1984) 81:3138-3142 Proc. Natl. Acad. Sci. U.S.A. (1984) 81:3138-3142 Proc. Natl. Acad. Sci. U.S.A. (1984) 81:3138-3142 Proc. Natl. Accession A22175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $26369 #type complete
genome polyprotein - eastern equine encephalomyelitis virus
nonstructural protein NS1; nonstructural protein NS2;
nonstructural protein NS3
nonstructural protein NS3
06-Jan = 1994 #sequence_revision 01-Nov-1996 #text_change
01-Nov-1996
                                                                                                                                                                                                                                                                                 ##molecule_type mRNA
##residues
##residues
81-120 ##label B12
##residues
81-120 ##sressed constitutively in occytes, disappears
NT This protein is expressed constitutively in occytes, disappears
after fertilization, and is induced by heat shock in somatic
cells from the gastrula stage onward.
IFICATION #superfamily heat shock protein 70
RDS #heat shock; molecular chaperone; stress-induced protein
RNS #length 647 #molecular-weight 70915 #checksum 3965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $18349  #type complete heat shock protein 70 carrot heat shock protein 70 carrot 4formal_name Daucus carot a frommon_name carrot 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 12-Apr-1995 $18349; $15514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross_references_EMBL.X60088
CLASSIFICATION #superfamily heat shock protein 70
SUMMARY #length 655 #molecular-weight 72051 #checksum 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Lin, X.; Chern, M.; Zimmerman, J.L.
#journal Plant Mol. Biol. (1991) 17:1245-1249
#title Cloning and characterization of a carrot hsp70 gene.
#cross-references MUID:92032789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Volchkov, V.E.; Volchkova, V.A.; Netesov, S.V. Mol. Gen. Mikrobiol. Virusol. (1991) 5:8-15
Complete nucleotide sequence of the eastern equine encephalomyelitis virus genome.
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Pred. No. 3.21e+00;
14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 84; DB 3; Length 647;
Pred. No. 3.21e+00;
12; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 erakrtlsssta-qttieidslyegvdfyttitrar 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
##residues 1-655 ##label LIN
                                                                                                       ##molecule_type DNA
##residues 1-647 ##label BIE
                                                                     #cross-references MUID:85076567
#accession A03310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.1%;
Best Local Similarity 30.6%;
Matches 11; Conservative
                                                    oocytes.
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KEYWORDS
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#title
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  #journal
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REFERENCE
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ORGANISM
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4
                                                                    sequence could not be checked because of bad print in
                                                                                                                                                       #product nonstructural protein NS1 #status predicted
#label NS1\
#product nonstructural protein NS2 #status predicted
#label NS2\
                                                                                                                                                                                                                                           #product nonstructural protein NS3 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   #checksum 5340
                                                                                                                                                                                                                                                                                                                            Query Match 13.1%; Score 84; DB 8; Length 1878; Best Local Similarity 33.9%; Pred. No. 3.21e+00; Matches 19; Conservative 14; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                       #molecular-weight 208582
                                                                                                             nonstructural protein; polyprotein
##molecule_type mRNA
##residues 1-1878 ##label VOL
##cross-references EMBL:X63135
                                                                                                                                                                                                                                                                #length 1878 #mo
                                                                                           paper
                                                                    ##note
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Aug 20 11:09:54 1997; MasPar time 3.60 Seconds 517.994 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-320-157-21 (1-88) from US08320157.pep 643 1 MASGQCPGPPRQECGKPALP......APWGRWDGSSPSPGRHQPAL 88 Title: Description: Perfect Score:

PAM 150 Gap 11 Scoring table:

Sequence:

59021 seqs, 21210388 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 swiss-prot34 Database:

Mean 38.620; Variance 68.467; scale 0.564 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.66e-02	3.58e-01	4.97e-01	6.89e-01	6.89e-01	6.89e-01	6.89e-01	6.89e-01	6.89e-01	6.89e-01	6.89e-01	6.89e-01	6.89e-01	9.52e-01	9.52e-01	9.52e-01	9.52e-01	9.52e-01	9.52e-01	9.52e-01	9.52e-01	1.31e+00
Description	HEAT SHOCK PROTEIN HT	70 KD PF	SHOCK 70 KD	SHOCK 70 KD	SHOCK 70 KD	HEAT SHOCK PROTEIN SS	HEAT SHOCK COGNATE PR	HEAT SHOCK PROTEIN SS	SHOCK 70 KD PF	SHOCK 70 KD	SHOCK 70 KD	SHOCK 70 KD	PROLINE-RIC	GOLIATH PROTEIN (G1 P	ALPHA-L-FUCOSIDASE PR	HEAT SHOCK 70 KD PROT	HEAT SHOCK 70 KD PROT	SHOCK 70 KD	SHOCK 70 KD	SHOCK PROTEI	ENDOTHELIAL ACTIN-BIN	HEAT SHOCK 70 KD PROT
А	HTGA_ECOLI	HS76_HUMAN	HS7D_DROME	HS7X_PIG	HS73_BOVIN	HS72_YEAST	HS7C_DICDI	HS71_YEAST	HS76_PIG	HS70_XENLA	HS70_BLAEM	HS70_DAUCA	BAT2_HUMAN	GOLI_DROME	FUCO_RAT	HS71_HUMAN	HS71_PIG	HS71_RAT	HS71 MOUSE	HS72_PICAN	ABP2_HUMAN	HS70 CHICK
88	Ŋ	S	S	Ŋ	ഗ	S	'n	Ŋ	S	ഗ	S	'n	Н	4	4	S	ß	S	ഹ	2	m	'n
Length	196	643	651	379	631	638	640	641	643	647	649	655	2142	284	462	641	641	641	642	642	2647	634
% Query Match	14.8	13.4	13.2	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.8
Score	95	98	82	84	84	84	84	84	84	84	84	84	84	83	83	83	83	83	83	83	83	82
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1.31e+00 1.31e+00 1.31e+00 1.31e+00 1.38e+00 1.80e+00 1.80e+00 1.80e+00 1.80e+00 2.47e+00 2.47e+00 2.47e+00 2.47e+00 2.47e+00 2.47e+00 3.38e+00 3.38e+00	3.38e+00
SHOCK CASE/PR CASE/PR CASE/PR CASE/PR CASE/PR SHOCK SH	HEAT SHOCK COGNATE 70
HS74_PARLI RYRIL HSVBC CALE_CHEV CALE_CHEV HS74_DROSI HS70_HONDY HS70_HONDA HS71_DROME HS71_DROME HS71_DROME HS71_DROME HS71_LYCES HS71_LYCES HS71_CANAL MYCR_HOMAN NYCR_HOMAN NYCR_HOMAN NYCR_ANDA HS71_ECOLI HS71_ECOLI HS72_HOMAN	HS/C_PETHY
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633 633 641 641 641 641 641 641 641 641	100
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ALIGNMENTS

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REALLINE; 9233497.

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RY JEDUROE JESUS SAN JEDUROE J
                                                                                                                                           01-DEC-1992 (REL. 24, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY).
HTGA OR HTPY.
ESCHERIACHA GOLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.
                                                             196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
STRAIN-K12 / W3110,
MEDLINE, 93239687.
MISSIAKAS D., GEORGOPOULOS C., RAINA S.;
J. BACTERIOL. 175:2613-2624(1993).
                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEBBAGE J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE; 94003405.
JAMES R., DEBN D.O., DEBB
DNA SEQ. 3:327-332(1993).
                                                        STANDARD;
RESULT 1
ID HTGA_ECOLI
AC P28697;
                                                             HID DESCRIPTION OF THE PROPERTY OF THE PROPERT
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GENE 128:155-163(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 AA;
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SEQUENCE FROM N.A.
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CONFLICT
CONFLICT
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
HEAT SHOCK 70 KD PROTEIN COGNATE 4 (HEAT SHOCK 70 KD PROTEIN 88E).
HSC4 OR HSC70-4.
DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
                                                                                                                                                                                                                                                                                                                                                                                                              HSPAG OR HSP70B'.
HOMO SAPIENS (HUMAN),
EUTHERIA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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BEDLINE; 93292982.
RUBIN D.W., MEHTA A., ZHU J., SHOHAM S., CHEN X., WELLS Q.,
PALTER K.B.;
                                                            Score 95; DB 5; Length 196;
Pred. No. 1.66e-02;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
13.4%; Score 86; DB 5; Length 643;
Best Local Similarity 26.8%; Pred. No. 3.58e-01;
Matches 11; Conservative 12; Mismatches 17: ThAPP
                                                                                                                                                                                                                                                                                                                        01-AGG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C., LIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 grlrtacerakrtlssstgatleidslfegvdfytsitrar 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 GPPRQECGKPALPSASEEQVAQDMEG-FSAATFFTTISRNR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-LUNG;
MEDLINE; 90226304.
LEUNG T.K.C., RAJENDRAN M.Y., MONFRIES C., HALL
BIOCHEM. J. 267:125-132(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIN: ILLUNCS, PRODEST, HSP70_1.
PROSITE; PS00329; HSP70_2.
PROSITE; PS01036; HSP70_3.
ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
SEQUENCE 643 AA; 70854 MW; D7C64887 CRC32;
                      D9E3CEC8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              651 AA.
                                                                                                                                                                                                                                                                                    643 AA
    POLY - SER
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                      21225 MW;
                                                                                                                                                      14 ppspaprskpcpstliaawvr 34
                                                                                                                                                                                 53 PPLPTQRWSPCPSNLAAPWGR 73
                                                                 h 14.8%;
Similarity 57.1%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-250 FROM N.A. MEDLINE; 92128997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P19120; 1NGA.
HSC-2DPAGE; P17066; HUMAN.
MIM; 140555; -.
PROSITE; PS00297; HSP70_1.
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                                                                                                                                                                                                                                                                                    STANDARD;
57
196 AA;
                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            RESULT 2

TD HS76_HUMAN
AC P1706;
DT 01-A0G-1990
DT 01-EB-1996
DE HEAT SHOCK 7
GN HSPA6 OR HSP
OS BUXARYOTA;
RN CC EUTHERIA; PR
CC EUTHERIA; PR
RN CC EUTHERIA; PR
RN EDLINE; 902
RA BEDCHEN. J. C. C.
RL BIOCHEN. J. C. C.
REBL; SS1758
DR REBL; SS1758
DR EMBL; SS1758
DR EMBL; SS1758
DR REBL; SS1758
DR REBL; SS1758
DR RESSP: P19120
DR ROSITE; PS0
DR PROSITE; PS0
DR ROSITE; PS0
KW ATP-BIRDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 3
HS7D_DROME
  DOMAIN
SEQUENCE
                                                                   Query Match
                                                                                                            Matches
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  단양
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Gaps
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EMBL; JO1500; G157661; -.
EMBL; J01500; G157665; -.
EMBL; J02569; G157655; -.
EMBL; J02569; G15778; ALT_SEQ.
PIR; A36333, A36333.
HSSP; P19120; JATR;
FLYBASE; F800001219; HSC70-4.
PROSITE; PS00129; HSP70_1.
PROSITE; PS00139; HSP70_2.
PROSITE; PS01036; HSP70_3.
ATP-BINDING; HEAT SHOCK; NUCLEAR PROTEIN; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEAT SHOCK 70 KD PROTEIN (FRAGMENT).
SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
[2] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE; 90258915.
PERKINS L.A., DOCTOR J.S., ZHANG K., STINSON L., PERRIMON N., CRAIG E.A.;
MOL. CELL. BIOL. 10:3232-3238(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.97e-01;
13; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 90371455.
BUCHMAN T.G., CABIN D.E., VICKERS S.;
SURGERY 108:559-566(1990).
EMBL; MILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; M29506, G164495; -.
HSSP; P19120; 1NGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 L -> P (IN REF. 2)
170 L -> P (IN REF. 2)
625 P -> G (IN REF. 2)
71131 MW; 75CC8721 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 rtacerakrtlssstgasleidslfegtdfytsitrar 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4

HGYX_PIG STANDARD; PRT; 379 AA.

AC 94934;
DT 01-FEB-1994 (REL. 28, CREATED)

DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)

DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)

DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00297; HSP70_1.
PROSITE; PS00329; HSP70_2.
PROSITE; PS01036; HSP70_3.
ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
NON_TER
                                                                                                                                                      SEQUENCE OF 1-104 FROM N.A.
MEDLINE, 84005511.
CRAIG E.A., INGOLIA T.D., MANSEAU L.J.;
DEV. BIOL. 99:418-426(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.3%;
Matches 10; Conservative
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ACETYLATION.
676F4EE3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
HSPB OR HSC70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
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                                                                                                                                                                  STRAIN-ATCC 38531 / Y41;
NORBECK J., BLOMBERG A.;
FEMS MICROBIOL. LETT. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69338 MW;
                                                                 SEQUENCE OF 91-97 AND 325-341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
13.1%;
Best Local Similarity 26.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD; L0002070; SSA2.
PROSITE; PS00297; HSP70_1.
PROSITE; PS00329; HSP70_2.
PROSITE; PS01036; HSP70_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUMYCETOZOA; DICTYOSTELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
    [3]
SEQUENCE OF 71-638 FROM
                                                                                                                                                                                                                                                                                                                                         PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SC01203; SSA2.
                                                                                                                                                         SEQUENCE OF 186-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPD; 9800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS7C_DICDI
P36415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INIT_MET
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LISTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                    RA SEQUENCE FROM N.A.

RA GROSZ M.D., MASSEY V.K., SKOW L.C.;

ROSZ M.D., MASSEY V.K., SKOW L.C.;

RE SEQUENCE FROM N.A.

RL SUBMITTED (XXX-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.

CC -I- FUNCTION: IN COOPERATION WITH OTHER CHAPRENGES, HSP70S STABILIZE PRESESSESTION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN OR ANGANELES. THESE CHAPRENONES PARTICIPATE IN ALL THESE PROCESSES CC OTHER PROTEINS. THES HOND EXCENSED PROTOFORMATIONS OF TYRONGCH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF OTHER PROTEINS. THESE STANSLODED PEPTIDE SEGMENTS WITH A NET CONFORMATION OR FOLLOWING STRESS-INDUCED DAMAGE.

CC -I- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.

DR EMBL, L10428 (31361); -.

DR FROSITE; PS00329; HSP70_1.

DR PROSITE; PS00329; HSP70_2.

DR PROSITE; PS01356; HSP70_2.

DR PROSITE; PS01356; HSP70_2.

EMBL, L10428 PSP70_2.

DR PROSITE; PS01356; HSP70_2.

DR PROSITE; PS01356; HSP70_2.
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                                                       ä
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                           BOS TAURUS (BOVINE).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84; DB 5; Length 631;
Pred. No. 6.89e-01;
15; Mismatches 17; Indels
                          Score 84; DB 5; Length 379;
Pred. No. 6.89e-01;
12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-S288C;
PURNELLE B., GOFFEAU A.;
SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 aparlrtacerakrtlssstgasieidslyegvdfytsitrar 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|: | : | :|:|:| | 6 GPGPPRQEGKPALPSASEEQVAQDMEG-FSAATFFTTISRNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEAT SHOCK PROTEIN SSA2.
SSA2 OR YLL024C OR L0931.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI: ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                            41
                                                                                        9E26ABE8 CRC32;
                                                                                                                                                                           01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (REL. 11, CREATED)
01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HEAT SHOCK PROTEIN SSA2.
                                                                        4 rtacerakrtlssstqatleidslfegvdfytsitrar
                                                                                                                                                      631 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288C;
MEDLINE; 89128457.
SLATER M.R., CRAIG E.A.;
NUCLEIC ACIDS RES. 17:805-806(1989).
                                                                                                                                                      PRT;
 42289 MW;
                         Query Match 13.1%;
Best Local Similarity 26.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.1%;
Best Local Similarity 23.3%;
Matches 10; Conservative
                                                                                                                                                                                                                  HEAT SHOCK 70 KD PROTEIN 3
                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                       EUTHERIA; ARTIODACTYLA
379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                               5
HS73_BOVIN
P34933:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HS72_YEAST
P10592;
 SEQUENCE
                                                                                                                                                                                                                                  HSP70-3
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GARRELS J. I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B.,
VOLPE T., WARNER J. S., MCLAUGHLIN C.S.;
SUBMITTED (SEP-1994) TO THE SWISS-PROT DATA BANK.
-I- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
ATP-DEPRINDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
SEQUENCE OF 71-638 FROM N.A.
DUESTERHOEFT A., FLOETH M., HEUSS-NEITZEL D., HILBERT H., MOESTL
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                             STRAIN-S28BC;
MEDLINE; 95203288.
GARRELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER VOLPE T., WARNER J.R., MCLAUGHLIN C.S.;
ELECTROPHORESIS 15:1466-1486(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-AX3;
MEDLINE: 94008983.
HAUS U., TROMMLER P., FISHER P.R., HARTMANN H., LOTTSPEICH F.,
NOEGEL A.A., SCHLEICHER M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ĥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLUAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL: X73297; G4546; -.
EMBL: X73297; B245749; -.
EMBL: X97560; E238712; -.
PIR; S20139; S20139.
HSSP: P19120; 1ATR.
SWISS-2DRAGE; P10592; XEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEAT SHOCK; ATP-BINDING; MULTIGENE FAMILY; ACETYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 84; DB 5; Len
Pred. No. 6.89e-01;
12; Mismatches 15;
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SUS SCROFA (PIG).
                                                                          MEDLINE; 95203288
                                                                                                                                                                                    ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT_MET
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 9
HS76_PIG
Q04967;
                                                                                                                                                                                                                                                                                                                                                                  (EPD; 97
                                                                                                                                                                                                                                                                                                                                                                             LISTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSP70B'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              合
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                                               MEDILIARY 344031110.

MEDDIA SAUTERER R.A., CONDEELIS J.S.;

J. BIOL, CHEM. 268:23267-23274(1993).

J. BIOL, CHEM. 268:23267-23274(1993).

-I- FUNCITON: AFRECTS ACTIN POLYMERIZATION THROUGH INTERACTION WITH ACTIN-BINDING PROTIEN CAPP32/34. ACTS AS A CHAPERONE BY STIMULATING THE REFOLDING OF DENATURATED CAP32 AND CAP34.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC. FOUND IN F-ACTIN-RICH REGIONS COF THE CELL CORTEX AND CELL PROTRUSIONS.

-I- DEVELOPMENTAL STAGE: HEAT SHOCK COGNATE PROTEINS ARE EXPRESSED CONSITIUTY VELY DURING NORMAL DEVELOPMENT.

-I- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.

REMBL; X75263; G433180; -.

-I- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.

REMBL; X75263; G433180; -.

REMBL; X75263; G433180; -.

REMBL; X75763; G433180; -.

REMBL; S37394; S37394.

REMBL; PS00227; HS970_1.

REMBL; PS00227; HS970_1.

REMBL; PS00329; HS970_3.
                                                                                                                                                                                                                                                                                                                                                                                                             ï
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                                                                                                                                                                                                                                                                     MSSIGIDLGTTYSCVGVWQNDRVEIIAND -> IHHHINGNATWVVESGPVSEVLSFN (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE; 9502815.
CLARK WH., KENG T., STORMS R.K., ZHONG W., FORTIN N., ZENG B.,
DELANK MS., OUELLETTE B.F.F., BARTON A.B., KABACK D.B., BUSSEY H.;
                      SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
                                                                                                                                                                                                                                                                                                                                                                                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                     Score 84; DB 5; Length 640;
Pred. No. 6.89e-01;
12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0TU-1989 (REL. 11, CREATED)
01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SSA1 OK YALOUSC.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                       N -> T (IN REF. 2).
N -> A (IN REF. 2).
R -> A (IN REF. 2).
S -> A (IN REF. 2).
V -> A (IN REF. 2).
V -> A (IN REF. 2).
F -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                262 rtacerakrtlsssagasieidslfegidfytsitrar 299
                                                                                                                                                                                                                                                                                                                                                                                                                                             641 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OGDEN R.C., LEE M.-C., KNAPP G.;
NUCLEIC ACIDS RES. 12:9367-9382(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89128457.
SLATER M.R., CRAIG E.A.;
NUCLEIC ACIDS RES. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                      237
240
341
352
70499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 590-641 FROM N.A. MEDLINE; 85087943.
                                                                                                                                                                                                                                                                                                                                                                                     y Match 13.1%;
Local Similarity 26.3%;
hes 10; Conservative
EMBO J. 12:3763-3771(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                      PROSITE; PSO0329; HSP7C
PROSITE; PSO1036; HSP7C
ATP-BINDING; CHAPERONE.
                                                                                                                                                                                                                                                                                                                                  240
341
352
352
640 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                           MEDLINE; 94043116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HS71_YEAST
P10591;
                                 STRAIN-AX3
                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                     CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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GARRELS J.I., FUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B., VOLPE T., WARNER J.R., MCLAGGHLIN C.S.;
SUBMITTED (SEP-1994) TO THE SWISS-PROT DATA BANK.
-!- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROTEINS IS EXECTED. SSA1 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                LATTER G.I., SCHWENDER B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAŽOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä
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01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEZEGRE F., VAIMAN M., CHARDON P.;
BIOCHINE, BIOPHYS. ACTA 1174:17-26(1993).
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; X12926; G312352; -.
EMBL; Z122015; G349747; ALT_SEQ.
PIR; S25438; HHBYAL.
PIR; S42164; S42164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEAT SHOCK; ATP-BINDING; MULTIGENE FAMILY; ACETYLATION
                       SLATER M.R.;
SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 84; DB 5; L
Pred. No. 6.89e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 rtacerakrtlsssaqtsveidslfegidfytsitrar 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ROECGKPALPSASEEQVAQDMEG-FSAATFFTTISRNR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 1 ACETYLATION.
641 AA; 69526 MW; 5B23162E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643 AA
                                                                                                                                                                                    GARRELS J.I., FUTCHER B., KOBAYASHI R.,
VOLPE T., WARNER J.R., MCLAUGHLIN C.S.,
ELECTROPHORESIS 15:1466-1486(1994).
                                                                                                                                                                                                                                                                                                     SEQUENCE OF 186-195.
STRAIN-ATCC 38531 / Y41;
NORBECK J., BLOMBERG A.;
FEMS MICROBIOL. LETT. 137:1-8(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
REVISIONS TO 207; 417 AND 421.
                                                                                                        SEQUENCE OF 91-97 AND 325-341 STRAIN-$288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P19120; 1NGJ.
SWISS-2DPAGE; P10591; YEAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.3*,
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD: L0002069; SSA1.
PROSITE; PS00297; HSP70_1.
PROSITE; PS00329; HSP70_2.
PROSITE; PS01036; HSP70_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J788; ... SC01202; SSA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
TISSUE-LYMPHOCYTES;
MEDLINE; 93326632.
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HSSP; P19120; 1NGJ.
PROSITE; PS00297; HSP70_1.
PROSITE; PS00329; HSP70_2.
PROSITE; PS01036; HSP70_3.
ATP-BINDING; HEAT SHOCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAT. GENET. 3:137-145(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAUCUS CAROTA (CARROT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   655 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 90192810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBELLIFERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 13
BAT2_HUMAN
P48634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HS70_DAUCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
1-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
1-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                                                                                                                                    / Match 13.1%; Score 84; DB 5; Length 643; Local Similarity 26.3%; Pred. No. 6.89e-01; nes 10; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; FUNGI; MASTIGOMYCOTINA; CHYTRIDIOMYCETES.
EMBL; X68213; G1978; -.
PIR; S25585; S25585.
PIR; S34625; S34625.
HSSP: P19120; 1NGI.
PROSITE; P800297; HSP70_1.
R PROSITE; P801036; HSP70_2.
R PROSITE; P801036; HSP70_3.
R ATP-BINDING; HEAT SHOCK; MULTIGENE FAMILY.
A12 AA: 71109 MW; 6F2B78FD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                       266 rtacerakrtlssstgatleidslfegvdfytsitrar 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 647 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 81-120 FROM N.A. MEDLINE; 84221917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIENZ M.;
EMBO J. 3:2477-2483(1984).
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MEDLINE; 95129910.
STEFANI R.M., GOMES S.L.;
GENE 152:19-26(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLASTOCLADIELLA EMERSONII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
HS70_XENLA
P02827;
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P48720;
                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE; 93272029.
IRIS F.J.M., BOUGGLERET L., PRIEUR S., CATERINA D., PRIMAS G.,
PERROT V., JURKA J., RODRIGUEZ-TOME P., CLAVERIE J.-M., DAUSSET J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                      Query Match 13.1%; Score 84; DB 5; Length 649; Best Local Similarity 26.3%; Pred. No. 6.89e-01; Matches 10; Conservative 12; Mismatches 15; Indels
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Pred. No. 6.89e-01;
14; Mismatches 9; Indels
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MEDLINE; 92032789.
LIN X., CHERN M., ZIMMERMAN J.L.;
PLANT MOL. BIOL. 17:1245-1249(1991).
-! SIMILARIY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; X60088; G18357; -.
PIR: S18349; S18349.
-i- SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY. EMBL, 122497; G773670; -. ATP-BINDING; CHAPENONE. SEQUENCE 649 AA; 70833 MW; 8ACFF56F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BANERJI J., SANDS J., STROMINGER J.L., SPIES T.;
PROC. NATL. ACAD. SCI. U.S.A. 87:2374-2378(1990)
                                                                                                                                                                                                                                                   267 rtacerakrtlsssaqtsleidslfegidfytsitrar 304
                                                                                                                                                                                                                                                                                72051 MW; 791B240F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
HEAT SHOCK 70 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                       655 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 2142 AA.
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PUTATIVE ROLE AS TRANSCRIPTION FACTOR.
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                                                                                                                                                                    ZN_FING
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        T 15
FUCO_RAT
P17164;
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BOUCHARD M.L., COTE S.;
GENE 125:205-209(1993).
-I- FUNCTION: REGULATION OF GENE EXPRESSION DURING MESODERM FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
               -1- TISSUE SPECIFICITY: LIMITED TO CELL-LINES OF LEUKAEMIC ORIGIN. BMJS. M33509; G179339; -. EMBL; M33518; G179345; -. EMBL; M33512; G179345; -. EMBL; M3512; G179345; -. EMBL; M3512; G179345; -. EMBL; C15025; G29375; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1281 apappraaakspdlsngnsdganeewetasessdftserrgdkeapppvlltpk 1334
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Pred. No. 6.89e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches 26; Indels
                                                                                                                                                                                GLN-RICH.
POLY-PRO.
POLY-PRO.
POLY-PRO.
POLY-GLY.
POLY-GLY.
POLY-PRO.
POLY-PRO.
POLY-PRO.
A X 57 AA TYPE A REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       2-2.
3 X 50 AA TYPE C REPEATS.
3-1.
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Q06003;

Q1-FEB-1994 (REL. 28, CREATED)

Q1-FEB-1995 (REL. 28, LAST SEQUENCE UPDATE)

Q1-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)

GOLIATH PROTEIN (G1 PROTEIN).

GOL OR G1. OR G1.

DROSOPHILA MELANOGASTER (FRUIT FLY).

EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
                                                                                                                                                                                                                                                                                                                                                                                      1-4.
2 X TYPE B REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2CFEF88A CRC32
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Best Local Similarity 27.8%;
Matches 15; Conservative
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2089
1948
2014
2089
 -! - FUNCTION: UNKNOWN
                                            EMBL, M33518; G179345
EMBL; M33512; G179345
EMBL; A15025; G29375;
PIR; B35098; B35098.
PIR; S36152; S36152.
MIM; 142580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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1285
1400
1611
1729
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                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                    REPEAT
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MEDLINE; 90147522.

FISHER K.J., ARONSON N.N. JR.;

BIOCHEM, J. 264:695-701(1989).

-!- FUNCTION: ALPHA-L-FUCOSIDASE IS RESPONSIBLE FOR HYDROLYSING THE ALPHA-L, 6-LINKED FUCOSE JOINED TO THE REDUCING-END N-ACETYLGLUCOSAMINE OF THE CARROHYDRATE MOIETIES OF GLYCOPROTEINS.
-!- CATALYTIC ACTIVITY: AN ALPHA-L-FUCOSIDE + H(2)O = AN ALCOHOL +
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATTUS NORVEGICUS (RAT).
BUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
BUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 29-40; 90-124 AND 307-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
ALPHA-L-FUCOSIDASE PRECURSOR (EC 3.2.1.51) (ALPHA-L-FUCOSIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBGNIT: HOMOTETRAMER.
-1- SUBCELLULAR LOCATION: LYSOSOMAL.
-1- SIMILARITY: BELONGS TO FAMILY 29 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA-L-FUCOSIDASE.
MAY BE IMPORTANT FOR CATALYSIS.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                            Score 83; DB 4; Length 284;
Pred. No. 9.52e-01;
16; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83; DB 4; Length 462;
Pred. No. 9.52e-01;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X16145; G55651; -.
PIR; S07074; S07074.
PIR; S10235; S10235.
PROSITE; PS00386; ALPHA_L_FUCOSIDASE.
HYDROLASE; GLYCOSIDASE: LYSOSOME; GLYCOPROTEIN; SIGNAL.
SIGNAL
                                                                                                                                                                                  208 259 GLN/PRO/SER-RICH.
284 AA; 31973 MW; FB98BE96 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
4923CBE4 CRC32;
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Best Local Similarity 46.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.3%;
Matches 15; Conservative
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm Wed Aug 20 11:12:02 1997; MasPar time 5.48 Seconds 438.125 Million cell updates/sec MPsrch_pp Run on:

Tabular output not generated.

Description: Title:

>US-08-320-157-22 (1-210) from US08320157.pep 1554 Perfect Score:

1 MASGQGPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 210

PAM 150 Scoring table:

Seguence:

96640 seqs, 11439865 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 a-geneseq27 Database:

Variance 141.622; scale 0.229 Mean 32.457; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Š.	-13	-13	-13	-13	-13	-96	-89	-71	-13	-13	-12	-12	-12	-12	-12	-12	-12	-12	-12	-12
	Pred.	4.01e-13	4.01e-7	.01e-	.36e-	.36e-1	1.82e-96	.42e-8	1.07e-	.49e-	.25e-	1.79e-	1.79e-	.95e-	.95e-	.43e-	.43e-1	.43e-1	.43e-1	.43e-	.43e-
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	Description	Bak protein.	Bcl-Y apoptosis-relat	Human Cdn-1.	Bak-2 protein.		Human Cdn-1(60-211).	Human Cdn-1(71-211).	Human Cdn-1(96-211).	Chicken lymphoid BCL	Apoptosis-blocking p	Human thymus BCL-XL.	Bcl-XL protein.	Apoptosis-blocking pa	Apoptosis-blocking pr	Human bcl-2 beta prot	Human thymus BCL-2.	Human bcl-2 protein.	Human bcl-2 alpha pro	Human oncogene bcl-2	Sequence of bc1-2-alp
	i 1																				
	Ω	W03668	R81451	R77876	W03669	R77877	R77879	R77880	R77881	R68884	W01020	R68887	W05821	W01019	W01018	R71405	R68886	R70332	R71404	R47344	P80987
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e Query	Match	99.3	99.3	99.3	97.2	97.2	73.1	68.3	9.99	16.6	16.5	16.1	16.1	15.8	15.8	15.6	15.6	15.6	15.6	15.6	15.6
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Result	No.	1	7	Ю	7	S	φ	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20

21 243 15.6 239 13 R70331 Human bcl-2 protein. 22 243 15.6 239 8 R42312 Bcl-2 oncogene produc 24 213 13.7 265 1 P80988 Squence of bcl-2 bct 25 204 13.1 205 19 R01021 Apoptosis blocking pr 26 203 13.1 202 19 W01021 Apoptosis blocking pr 27 194 12.5 350 12 R68814 Human Bax protein. 28 179 11.5 350 12 R68814 Human mcl-1 gene prod 30 6.3 177 14 R76996 Human thymus BcL-XI. 31 97 6.2 170 13 R68888 Human thymus BcL-XI. 32 43 19 W05298 Exterase secretory pr 34 6.0 338 14 R73955 Duffy blood group gpD 35 89 5.7 277 14 R74737 ACT-4 cell surface re 36 89 5.7 277 14 R79163 Human mclura. 37 88 5.7 277 14 R79163 Human mclura. 38 88 5.7 277 14 R79163 Human mclura. 39 88 5.7 277 14 R79163 Human mclura. 41 88 5.7 2092 Human mclura. 42 87 5.6 451 14 R70909 N. crassa mtr gene pr 43 87 5.6 1984 18 R99639 Peripheral nervous sy 45 198 18 87 2713 W00168 Human Trotein of Neuros	7.43e-12 3.14e-09 3.14e-09 1.88e-08 1.36e-08 1.36e-04 6.50e-04 6.50e-04 6.50e-04 7.50e-00 9.35e+00 9.35e+00 9.36e+01 3.10e+01 3.10e+01 3.64e+01 3.64e+01 3.64e+01 3.64e+01 3.64e+01 3.64e+01 3.64e+01 4.27e+01 4.27e+01
243 15.6 239 13 213 13.7 288 13 204 13.1 208 13 204 13.1 192 13 190 13.1 192 13 179 11.5 350 12 170 11.5 6.2 170 13 97 6.2 170 13 96 6.2 170 13 96 6.2 443 19 96 6.2 443 19 97 6.2 170 13 89 5.7 274 14 89 5.7 277 14 88 5.7 271 14 88 5.7 269 218 88 5.7 271 14 88 5.7 269 218 88 5.7 269 218	Human bc1-2 protein. Bc1-2 oncogene produc Human Cdn-3. Sequence of bc1-2-bet Murine Bax protein. Apoptosis-blocking pr Human Bax protein. Human mc1-1 gene prod Human mc1-1 gene prod Human hymus BCL-XI. Deduced sequence enco Human thymus BCL-XI. Esterase Secretory pr Duffy blood group gpD Inositol-3-phosphate ACT-4-61 surface re ACT-4-61 receptor se Partial sequence of b Human mG1uR4. Human mG1uR4. Human mG1uR4. Human T cell inositol N. crassa mtr gene pr Mtr protein of Neuros Peripheral nervous sy Peripheral nervous sy
243 15.6 239 1 213 13.7 288 1 204 13.1 192 1 194 1 195	R70331 R42312 P80988 P80988 R71407 W01002 R68814 R68816 R6888 R6888 R6888 R73559 R73559 R73558 R73558 R73558 R73558 R73558 R73559 R7355
243 22133 22133 15.6 2014 115.6 1179 1179 1179 1179 1179 1179 1179 117	138 138 140 110 110 110 110 110 110 110
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ALIGNMENTS

Compounds which This Bak protein sequence represents a bcl-1 homologue which inties Bak protein sequence represents a bcl-1 homologue which interacts with Epstein Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which hibbit the interaction may be used as virucide, antitumour or an antibody; Human; Bak; apoptosis; latency; virus replication; Epstein: Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; immunoassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic. Screening for anti-viral agents - by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral T 1 W03668 standard; Protein; 211 AA. 19-APR-1996; U05639. 20-APR-1995; US-426529. (LXRB-) LXR BIOTECHNOLOGY INC. 22-FEB-1997 (first entry) Barr PJ, Kiefer MC; WPI; 96-485886/48. diagnostic agents. N-PSDB; T42138. Homo sapiens Bak protein. 24-OCT-1996 RESULT NAME OF THE PROPERTY OF THE PR

Length 211; Indels Score 1543; DB 20; Pred. No. 4.01e-136; 0; Mismatches 0; 99.3%; larity 99.5%; Conservative Query Match Best Local Similarity Matches 210; Conser

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Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
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20-APR-1995; US-426529.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                            30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-CCT-1994; US-320157.
(LARB-) LAR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 4
W03669 standard; Protein; 211
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Best Local Similarity 99.5%;
Matches 210; Conservative
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WPI; 96-485886/48.
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WPI; 95-215106/28.
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                             Human Cdn-1.
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N-PSDB; T17375.
New isolated human Bcl-Y protein - used to develop prods. for
treating disorders characterised by inappropriate cell proliferation
or cell death.
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Bcl-Y protein (R81451) is a member of the Bcl-2 family and can induce apoptosis in cells and function as a negative regulator of Bcl-2 function. Bcl-Y mRNA was detected in all human tumour cell lines examined and is also widely expressed in primary human tissues. It can be obtd. by expression of a full-length cDNA clone (T1735) in pref. mammalian host cells. Bcl-Y can be used to develop prods. for treating disorders associated with inappropriate cell proliferation or cell death, and to raise antibodies used for the diagnosis or monitoring of such disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                Query Match 99.3%; Score 1543; DB 17; Length 211; Best Local Similarity 99.5%; Pred. No. 4.01e-136; Matches 210; Conservative 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                          R01451;
02-JUL-1996 (first entry)
Bcl-Y apoptosis-related protein.
Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label~ C-terminal_domain
/note~ "putative membrane localisation sequence"
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                                                                                                                                                                                                                                                            180 LNLGNGPILNVLVVLGVVLLGQFVVRRFFKS 210
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ID R77876 standard, Protein, 211 AA.
AC R77876,
                                                                                                                                                                                                                                                                                                                                                                                               R81451 standard; Protein; 211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-1995; U10103.
09-AUG-1994; US-287427.
11-OCT-1994; US-321071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMU-) IMMUNOGEN INC. Chittenden TD;
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61 vtlplqpsstmgqvgrqlai1gddinrrydsefqtmlqhlqptaenayeyftk1atslfe 120
New nucleic acid sequences encoding cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                             Disclosure; Fig. 3A-B; 66pp; English.

Cdn-1 cDNA was isolated from a human heart cDNA library using a previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HT29 cells. Expression of cdn-1 in WT-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MASGOGPGPPROECGEPALPSASEEQVAQDTEEVFRSYVFYRHQQEQEAEGVAAPADPEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       masgqgpgpprqecgepalpsaseeqvaqdteevfrsyvfyrhqqeqeaegvaapadpem
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This Bak-2 protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Bak-2; apoptosis; latency; virus replication;
Epstein-Barr virus; BHRF1; fusion protein; epitope tag;
drug screening; co-precipitation; ELISA; immunoassay; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein interactive trapping; virucide; antitumour; diagnostic. WO9633416-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for anti-viral agents – by detecting the ability of agent to disrupt the interaction of a Bak protein and a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1543; DB 13;
Pred. No. 4.01e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 LNLGNGPILNVLVVLGQVVLLGQFVVRRFFKS 210
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w09515084-A.
08-JUN-1995.
30-NOV-1994; U13930.
30-NOV-1993; US-160067.
07-0CT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1995.
30-NOV-1994; UJ3930.
30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R77880 standard; Protein; 141
R77880;
                                                                                                                                                                                                                                                                                                                                     standard; Protein; 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 73.1%;
Local Similarity 99.3%;
les 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shock; lymphoma; eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kiefer MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barr PJ, Kiefer MC; WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human Cdn-1(60-211)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Cdn-1(71-211)
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WPI; 95-215106/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
W09515084-A.
                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                             R77879;
                                                                                                                                                                                                                                                                                                       T 6
R77879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 vtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiasslfe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sginwgrvvallgfsyrlalhiyqrgltgflgqvtrfvvdfmlhhciarwiagrggwvaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 vtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiasslfe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak-2 protein and a viral protein (e.g. EBV BRRFI), exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak-2 and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 masgggpgpprqecgepalpsaseeqvaqdteevfrsyvfyhhqqeqeaegaaapadpem 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 masgagppppraecgepalpsaseeqvaqdteevfrsyvfyhhqqeqeaegaaapadpem 60
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 etc.
Disclosure; Fig.5D-E; 66pp; English.
Cdn-2 cDNA was isold. from a human placental genomic library
using a 950 bp fragment of Cdn-1 cDNA. Expression of Cdn-2
in mouse progenitor B-cell Fi5.12 cells decreased IL-3-induced
appropsis. The Cdn-2 protein displayed 97% amino acid identity
with Cdn-1 (R7/876).
Sequence 211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                            ;;
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                                                                                                                                                                                                                                                                                                                               Length 211;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                            97.2%; Score 1511; DB 20; 96.7%; Pred. No. 5.36e-133;
                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
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30-NOV-1993; US-160067.
70-CT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity 96.7%;
les 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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WPI; 95-215106/28.
N-PSDB; Q95493.
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Matches 204; Conser
                                                                                                                                                                                                                                    diagnostic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-1995.
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig.11; 66pp; English.

Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly decreased this activity, suggesting that small, truncated Cdn-1 sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 mvtlplqpsstmgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiatslf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV, autoimmune disease; reperfusion injury; hepatitis, osteoporosis; shock; lymphoma; eczema.
                                                                                                                                                                                                                                                                                                                                        Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV
autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequences encoding Cdn apoptosis modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1136; DB 13;
Pred. No. 1.82e-96;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
                                                                                          181 Inlgngpilnvlvvlgvvllggfvvrrffks 211
                                                                                                                        180 LNLGNGPILNVLVVLGVVLLGQFVVRRFFKS
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Sequence

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New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. neuronal cells, lymphocytes and cancers claim 4; Page 87; 127pp; English.

This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures.

The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic lateral sollerosis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 eqvvnelfhdgvnwgrivaffsfggalcvesvdkemrvlvgrivswmttyltdh-ldpwi 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 vvngatvhrsslevheivrasdvrgalrdagdefelryrrafsdltsglhitpgtaygsf 119
                                             Chicken lymphoid BCL-X.
Chicken; bird; fowl; BCL-X; apoptosis; cell death; cancer;
neurodegenerative disease; autoimmune disease; Parkinson's disease;
amylotrophic lateral sclerosis; multiple sclerosis; oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEI; 96.427035/43.

Nucleic acids encoding apoptosis regulating proteins - useful for diagnosing and treating immune disorders, malignancies, etc.
diagnosing and treating immune disorders, malignancies, etc.
Example 8; Page 34.35; 60pp; English.
The 80-6 mutant (W01020) of the bcl-2 oncogene product (W01018) lacks amino acids 80-86 of the native protein. This and other Bcl-2 mutants (see also W01019-21) were used in a two hybrid assay to examine the interactions between Bcl-2 and novel apoptosis-regulating proteins Nipl, Nip2 and Nip3 (W00997-99). 2 Motifs (W01003-04) on Bcl-2 were identified that are essential for interaction with the Nip proteins. These motifs show homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis-blocking protein Bc1-2 mutant 80-6 (de180-86).
Apoptosis-regulating protein; Bc1-2; oncogene;
adenovirus E1B 19k protein; cell death; cancer; tumour;
immune disorder; diagnosis; therapy; Bipla; Bip13; Bip5; NIp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 258; DB 13;
Pred. No. 3.49e-13;
32; Mismatches 59
                                                                                                                                                                                                                                                                                                 Thompson CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W01020 standard; Protein; 232 AA.
W01020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.6%;
28.2%;
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 28.2%;
les 37; Conservative
                                                                                                                                                                                                     22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1996.
21-MAR-1996; 104542.
21-MAR-1995; US-408095.
(UYSL-) UNIV ST LOUIS.
                                                                                                                                                                                                                                                                                            Boise LH, Nunez G,
WPI; 95-052079/07.
N-PSDB; Q81696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 AA;
                                                                                                                                         Gallus domesticus.
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                                                                                                                                                            WO9500642-A.
                                                                                                                                                                                     05-JAN-1995.
                           10-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 MGQVGRQLAIIGDDINRRYDSEFQIMLQHLQPIAENAYEYFTKIAISLFESG-NWGRVVA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ligfgyrlalhvyqhgltgflgqvtrfvvdfmlhhciarwiaqrggwvaalnlgngpiln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          w nucleic acid sequences encoding Cdn apoptosis modulators - and lated vectors, transformed cells, proteins and antibodies, useful diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                                                                                                                                                                                                                                                                                          1 mgqvgrqlaiigddinrrydsefqtmlqhlqptaenayeyftkiatslfesginwgrvva 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences encoding cdn apoptosis modulators - and related vectors, transformed cells, proteins and antibodies, useful or diagnosis and treatment e.g. of HIV infection, reperfusion injury
                                                                                  Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Res-mediated apoptosis. Deletion of the N-terminal 70 amino acids of Cdn-1 improved this activity, suggesting that small, truncated Cdn-1 molecules may be potent therapeutics.
                                                                                                                                                                                                                                                                                                                 Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas mediated apoptosis. Truncated Cdn-1 derivatives given in R77879-81 were used to test the effects of deleting the N-terminal sequences of Cdn-1 on this activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 rfvvdfmlhhciarwiaqrggwvaalnlgngpilnvlvvlgvvllgqfvvrrffks 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV; autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                   Score 1061; DB 13; Length 141;
Pred. No. 3.42e-89;
0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 880; DB 13; L
Pred. No. 1.07e-71;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .r 8
R77881 standard; Protein; 116 AA.
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ID R68884 standard; Protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 VLVVLGVVLLGQFVVRRFFKS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 vlvvlgvvllgqfvvrrffks 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1993; US-160067.
07-OCT-1994; US-320157.
(LXRB-) LXR BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.6%;
                                                                                                                                                                                                                                                                   Query Match 68.3%;
Best Local Similarity 99.3%;
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.1%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1995 (first entry)
Human Cdn-1(96-211).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shock; lymphoma; eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barr PJ, Kiefer MC;
WPI; 95-215106/28.
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R77881;

115;

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Seguence Query Match

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Indels

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Inducting or preventing death of T cells by bcl-XL protein regulation

"used to increase survival of HIV infected cells or to
down.regulate immune responses in immune diseases

Disclosure; Page 52-53; 76pp; English.

This is the sequence of a human bcl-XL protein, which protects
T-lymphocytes against cell death. A splice variant form, bcl-XS,
lacks a stretch of 63 amino acids, and is a dominant negative
regulator of 6bcl-XL function. The gene may be modified to
facilitate interaction with costimulatory Bax protein and inhibit
interaction with antagonistic Bad protein, by modification of the
Bcl-2 homology domains BHI and/or BH2. The bcl-XL gene may be
controduced into T-cells in vivo or ex vivo via gene transfer using
a vector for HIV infection gene therapy, to augment intracellular
continuous interaction and protect from cell death. A corresponding
antisense oligonuclectide or expression vector may be used in gene
therapy of e.g. autoimmune disease, graft rejection or graft.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 dspavngatghs-ssldarevipmaavkqalreagdefelryrrafsdltsqlhitpqta 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndh-l 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 EAEGVAAPADPEMVTLPLQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis-blocking protein Bcl-2 mutant 42-8 (del42-48). Apoptosis-regulating protein; Bcl-2; oncogene; adenovirus ElB 19K protein; cell death; cancer; tumour; immune disorder; diagnosis; therapy; BiplA; BiplA; Bipl5; NIpl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         down-regulate the immune response in a T-lymphocyte population
Bcl-XL protein.

Human; bcl-XL; T-lymphocyte; cell death; BH1 domain; BH2 doma
Bcl-2 homology domain; gene therapy; HIV; AIDS; antisense;
immune disorder; autoimmune disease; graft rejection;
graft-versus-host disease; apoptosis; adoptive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match
Local Similarity 25.5%; Pred. No. 1.79e-12;
les 36; Conservative 41; Mismatches 60: Indels
                                                                                                                           Location/Qualifiers
129..148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .T 13
W01019 standard; Protein; 232 AA.
W01019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || : ||| : ::| || :
167 ARWIAQRGGWVAALNL-GNGP 186
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                                                                                                                                                                                      180..191
                                                                                                                                                                                                                                                                    02-MAY-1996; U06203.
04-MAY-1995; US-435518.
07-JUN-1995; US-4435518.
(ARCH-) ARCH DEV CORP.
(USNA) US SEC OF NAVY.
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(UXSL-) UNIV ST LOUIS.
                                                                                                                                                                                                                                                                                                                                                                            Thompson CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-1996; 104542.
                                                                                                                                                                                                       /note= "BH2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 AA;
                                                                                                                                                                /note- "BH1 domain
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 96-506159/50.
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                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                     07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nip2; Nip3.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 ffssgpghtphp-aasrdpvartsplqtpaapgspvppvvhltlrgagddfsrryrrdfa 106
                                                                                                                                                                                                                                            61 dspavngatghs-ssldarevipmaavkgalreagdefelryrrafsdltsglhitpgta 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndh-1 178
                                                                                                                                                                                                                                                                                        95 TMLOHLOPTAENAYEYFTKIATSLFESG-NWGRVVALLGFGYRLALHVYQHGLTGFLGQV 153
                                                                                                                                                                                            40 FYRHQQEQEAEGVAAPADPEMVTLPLQPSSTMG-QVGR--QLAI--IGDDINRRYDSEFQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. claim 3; Page 94; 127pp; English.

This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures. The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic lateral sclerosis and multiple sclerosis.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                           6
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Pred. No. 1.79e-12;
41; Mismatches 60; Indels (
                                                                                    Length 232
to motifs (W01005-06) identified on the adenovirus ElB 19K
                                                                              Score 256; DB 19;
Pred. No. 5.25e-13;
40; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                           167 alwmteylnrh-lhtwigdnggwdafvel-ygpsmrpl 202
                     apoptosis-blocking protein (W01010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boise LH, Nunez G, Thompson CB; WPI; 95-052079/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          R68887 standard; Protein; 233 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCL-XL; apoptosis; cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 epwiqenggwdtfvelygnna 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.1%;
Best Local Similarity 25.5%;
Matches 36; Conservative
                                                                            Match 16.5%;
Local Similarity 29.7%;
les 47; Conservative
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22-JUN-1994; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human thymus BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple sclerosis.
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WO9500642-A.
                                           Sequence
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                                                                                  Query Match
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RESULT ID WO AC WO DT 30

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NOT COULD CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                     diagnosing and treating immune disorders, malignancies, etc.

Example 8; Page 33-34; 60pp; English.

The 42-8 mutant (Wollo19) of the bcl-2 encogene product (Wollo18)

Lacks amino acids 42-48 of the native protein. This and other

Bcl-2 mutants (see also Woll020-21) were used in a two hybrid assay

to examine the interactions between Bcl-2 and novel apoptosis-

requiating proteins Nipl. Nipl and Nipls (WO0997-99). The Nip

proteins were unable to interact with mutant 42-8. The site of

deletion in this mutant corresponds to a motif (see also Woll003)

C blinding motif (Woll004) of Bcl-2 was also identified, and both

show homology to motifs (Woll005-06) found on the 19K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 tvvoelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-1996; 104442.

21-MAR-1996; 104-00095.

A (UYSL-) UNIV ST LOUIS.

Chinadurai G;

(UYSL-) UNIV ST LOUIS.

Chinadurai G;

WIY, 96-427055/43.

Total diagnosing and treating immune disorders, malignancies, etc.

3. Example 8; page 32-33; 60pp; English.

The bol-2 oncogene product (W01018) enhances the survival of haematopoietic B and T cells by blocking apoptosis induced by Chicage agents. Its activity is similar to that of the 19K protein (W01010) of adenovirus Elb. 3 Novel proteins, Bipla, Elb. 3 Novel proteins, Bipla, Bipla, and Bip5 (W01000-02), that specifically interact with Elb. 3 howes the apoptosis-regulating Nup proteins (see also W01019-21) shows the apoptosis-regulating Nup proteins (see also W01019-21) shows the apoptosis-regulating Nup proteins (see also W01019-31) shows the apoptosis-regulating Nup proteins (see also W01013-04) that show homology to motifs (W01005-06) on 19K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargcfa 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps

    useful for

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis blocking protein Bcl-2, Apoptosis regulating protein; Bcl-2; oncogene; adenovirus ElB 19K protein; cell death; cancer; tumour; immune disorder; diagnosis; therapy; Bipla; Bipl3; Bip5; NIP1;
Chinnadural G; WPI; 96-427055/43. Nucleic acids encoding apoptosis regulating proteins - usefu vicieic acids encoding apoptosis regulating proteins - usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 245; DB 19; Length 232;
Pred. No. 4.95e-12;
36; Mismatches 57; Indels (
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/note= "interacts with Bip proteins"
EP-733706-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binding_site 43..51
/label~ Binding_motif
/note⇔ "interacts with Bip proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W01018 standard; Protein; 239 AA.
W01018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     15.8%;
Local Similarity 29.3%;
les 41; Conservative
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While you producing and identifying mutant bel-2 proteins -
that lack death repressor activity and/or lacks binding to Bax.

PD Soloclosure; Page 40; 133pp; English.

Ensemble of the proteins respectively. bel-2 is encoded by a prote-oncogene and is capable of inhibiting apoptosis in many hematopoietic cell systems.

CC bel-2 is a 26 kn membrane-associated cytoplasmic protein and is thought to function by enhancing the survival of hematopoietic cells of B and T co function by enhancing the survival of hematopoietic cells of B and T co rigins rather than directly promoting proliferation of these cell cytoplasmic protein and is thought cc origins rather than directly promoting proliferation of these cell cytoplasmic protein by enhancing the survival of hematopoietic cells of B and T correston nor does it necessarily alter the dose reponse to limiting concentrations of IL-3. bel-2 has been shown to form heterodimers with a protein, Bax. Overexpressed Bax accelerates apoptotic cell death concentration of between bel-2 and Bax determines cell survival or death of callowing an apoptotic stimulus. The invention gives a mutant form of following an apoptotic stimulus. The invention gives a mutant form of concentration of bel-2 in which there is at least one amino acid substitution or deletion in the BHI or BH2 domains. This makes the mutant protein substantially concentral and aliminaring and promose in animinarium service bown regulation of bel-1 is useful in cancer therapy, controlling hyperaple of hinding an apoptory and promose in animinarium services and animinarium service concentration of persons activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyperplasts and eliminating self-reactive clones in autoimmunity by favouring death effector molecules. Up regulating bcl-21s beneficial in treatment and diagnosis of immunodeficiency diseases, including AIDS and neurodegenerative and ischaemic cell death.

Sequence 205 AA;
                                                                                                                                                                                                   132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 190
                                                                                                                                                  74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargcfa 131
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bc1-2 beta protein.

Human, bc1-2; alpha; beta; proto-oncogene; hematopoietic cell line; apoptosis; membrane-associated cytoplasmic protein; B cell; T cell; proliferation; cell cycle progression; Bax; apoptotic cell death; apoptosis; cytokine; death repressor; BHI; BH2; cancer therapy; hyperplasia; immunodeficiency disease; AIDS; neurodegeneration; ischaemic cell death.
                                                                             .
9
Length 239;
                                                                             Mismatches 57; Indels
                                Pred. No. 4.95e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- BH2_domain
/note- "Represents Bax binding site"
W09505750-A.
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136..155
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                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 dnggwdafvel-ygpsmrpl 209
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172 QRGGWVAALNLGNGPILNVL 191
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                                                                         41; Conservative
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(UNIW ) UNIV WASHINGTON.
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US-248819.
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26-AUG-1993; US-112
                        Best_Local Similarity
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95-106605/14.
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Length 205;

Score 243; DB 13; Pred. No. 7.43e-12;

15.6%;

- g &
- 191 dnggwvga 198 : ||||:| 172 QRGGWVAA 179

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Search completed: Wed Aug 20 11:12:27 1997 Job time : 25 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Aug 20 11:12:45 1997; MasPar time 9.69 Seconds 626.144 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-320-157-22 (1-210) from USO8320157.pep 1554 1 MASGGCPGPPRQECGEPALP......LVVLGVVLLGQFVVRRFFKS 210 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

pir51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Mean 45.070; Variance 107.726; scale 0.418 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMARIES		
Result No.	Score	Query Match	Length	DB	e e	Description	Pred. No.
1	1543	99.3	211	13	S58873	Bak protein - human	1.46e-241
7	1511	97.2	211	13	S58875	cdn-2 protein - huma	6.54e-236
m	258	16.6	190	13	A47537	ula	6.91e-22
4	254	16.3	233	14	S51761	BCL-X protein - rat	2.79e-21
Ŋ	254	16.3		14	149056	OE	2.79e-21
9	250	16.1		13	B47537	apoptosis requlator	1.13e-20
7	247	15.9		14	149057	bcl-x transmembrane	3.19e-20
ω	246	15.8		9	B37332	transforming protein	4.51e-20
σ	245	15.8		9	A37332		6.38e-20
10	243	15.6		~	TVHUB1		1.27e-19
11	239	15.4		φ	D37332	transforming protein	5.07e-19
12	239	15.4		7	TVHUA1		5.07e-19
13	236	15.2		14	167431		1.42e-18
14	234	15.1		~	TVMSB1	transforming protein	2.83e-18
15	234	15.1		~	TVMSA1		2.83e-18
16	234	15.1		ဖ	E37332		2.83e-18
17	231	14.9		14	167432	$\overline{}$	7.90e-18
18	223	14.4	232	9	S24390	transforming protein	1.21e-16
19	202	13.2	192	14	D47538	programmed cell deat	5.11e-14
20	194	12.5	192	13	A47538	bcl-2-associated pro	1.93e-12
21	189	12.2	218	13	B47538	bcl-2-associated pro	9.88e-12

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ALIGNMENTS

RESULT 1	050073 # + **********************************
TITLE	Sak protein - himan
ALTERNATE_NAMES	bcl-2 homolog; cdn-1 protein
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 06-Sep-1996
ACCESSIONS	S58873; S58872; S58874
	S58873
#authors	Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington,
#journal	C.; Lutz, R.J.; Evan, G.I.; Guild, B.C. Nature (1995) 374.733-736
#title	Induction of apoptosis by the Bcl-2 homologue Bak.
#accession	S58873
##status	preliminary; nucleic acid sequence not shown
##molecule_type mRNA	type mRNA
##residues	1-211 ##label CHI
##Cross-rei	##Cross-relerences EMBL:U23765
#authore	5000/2 Parrow S N · White I H M · Martinon I · Dayon P · Din
	Grinham, C.J.; Martinou, J.C.; Brown, R.
#journal	Nature (1995) 374:731-733
#title	Cloning of a bcl-2 homologue by interaction with adenovirus
#accession	S58872
##status	preliminary
##molecule_type mRNA	type mrna
##residues	1-211 ##label FAR
##cross-ref	##cross-references EMBL:X84213
REFERENCE	S58874
#authors	Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky,
*******	S.R.; Tomei, L.D.; Barr, P.J.
#journar #title	Macure (1993) 3/4:/30-/33 Modulation of apoptosis by the widely distributed Bcl-2
	homologue Bak.
#accession	S58874
##status	preliminary
##molecule_type mRNA ##residnes 1-21	type mrnA 1-211 ##]ahal kir
##Cross-ref	_
GENETICS	
#gene	ne GDB:BAK-LSB
SUMMARY	erences gub:03300/ #length 211 #molecular-weight 23409 #checksum 801

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Nature (1995) 374:736-739
Modulation of apoptosis by the widely distributed Bcl-2
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#formal_name Gallus gallus #common_name chicken
03-May-1994 #sequence_revision 03-May-1994 #text_change
03-May-1994
A47537
                                                            Gaps
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cdn-2 protein - human
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15-Feb-1996 *sequence_revision 01-Mar-1996 #text_change
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5; Mismatches 1;
  Score 1543; DB 13;
Pred. No. 1.46e-241;
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larity 99.5%;
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Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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bcl-x, a bcl-2-related gene that functions as a dominant
regulator of apoptotic cell death.
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#length 233 #molecular-weight 26130
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#length 190 #molecular-weight 21467
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Pred. No. 6.91e-22;
32; Mismatches 59;
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##cross-references EMBL:X82537
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Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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#journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in and T lymphocytes.
#cross-references WUID:95052604
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bcl-x, a bcl-2-related gene that functions as a dominant
regulator of apoptotic cell death.
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submitted to the EMBL Data Library, November 1994
IL-5 inhibits anti-IgM-induced apoptosis in an immature l
call line through inductin of bcl-XI.
$52866
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Pred. No. 2.79e-21;
41; Mismatches 60; Indels 4; Gaps
               bcl-x long - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
15-Oct-1996
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#formal_name Homo sapiens #common_name man
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##cross-references EMBL:X83574
X #length 233 #molecular-weight 26132 #checksum 5739
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##cross-references EMBL:U10101; NID:g506647; CDS_PID:g506648
NCE S52866
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#title Cloning and molecular characterization of mouse bcl-x in and T lymphocytes.
#cross-references MUID:95052604
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##residues 1-21/ 4.2...
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Best Local Similarity 25.5%; Pred. No. 1.13e-20;
Matches 36; Conservative 41; Mismatches 60; Indels
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##molecule_type mRNA
##residues 1-69,'G',71-125,189-233 ##label BO2
##cross-references GB:L20122; CDS_PID:g623237
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bcl-x transmembrane deleted - mouse
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Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
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                                                                                                      Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene
expression in a variety of fissues including lymphoid
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#formal_name Gallus gallus #common_name chicken
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Pred. No. 4.51e-20;
37; Mismatches 56; Indels
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Pred. No. 6.38e-20;
40; Mismatches 57; Indels
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Local Similarity 28.5%;
Ge 39; Conservative
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A37332; S35453
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#authors Tsujimoto, Y.; Croce, C.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products
of bcl-2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
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#map_position 18q21.33-18q21.33
CLASSIFICATION #superfamily bol transforming protein
KEYWORDS alternative splicing; B-cell lymphoma; follicular lymphoma;
transforming protein
transforming protein
#length 205 #molecular-weight 22182 #checksum 1183
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expression in a variety of tissues including lymphoid an
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#formal_name Homo sapiens #common_name man
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
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#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
#title Analysis of the structure, transcripts, and protein products
    of bcl.2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
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S.; Goldman, P.; Korsmeyer, S.J.
#journal EMBO J. (1988) 7:123-131
#title Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2--Ig fusion gene in lymphoma.
#cross-references MUID:88196071
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#title Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: deregulated expression of a chimeric and mutated BCL-2 gene.
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54 APADPEMVTLP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT 112
                                     133 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwig 191
                                                        113 KIATSLFESG-NWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHHCIARWIA 171
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Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid a
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#authors Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
#journal Endocrinology (1995) 136.232-241
#title Expression of members of the bol-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bol-2 and bol-xlong messenger ribonucleic acid levels.
#accession 167431
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#superfamily bcl transforming protein
alternative splicing; B-cell lymphoma; follicular lymphoma;
prote-oncogene; transforming protein
#length 239 #molecular-weight 26266 #checksum 8323
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sidues 1-6,'S',8-58,'T',60-128,'C',130-239 ##label HUA2 to the sequence was determined from the germine gene constitutive expression of BCL2 following t(14:18) chromosomal translocation is typically found in follicular lymphoma.
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Pred. No. 1.42e-18;
30; Mismatches 50; Indels 3; Gaps
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transforming protein bcl-2-beta - mouse
#formal_name Mus musculus #common_name house mouse
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
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Pred. No. 5.07e-19;
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#map_position 18q21.33-18q21.33
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Best Local Similarity 28.4%;
Matches 33; Conservative
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Best Local Similarity 29.3%;
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#journal Cc11 (1987) 49:455-463
#title Molecular analysis of mbc1-2: structure and expression of the muthing gene homologous to the human gene involved in follicular lymphoma.
#cross-references MUID:87187643
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                                                  Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
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Nogrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
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#title Molecular analysis of mbcl-2: structure and expression murine gene homologous to the human gene involved in follicular lymphoma.
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Pred. No. 2.83e-18;
28; Mismatches 41; Indels
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##residues 1-236 ##label NEG
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##residues 1-199 ##label NEG
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Best Local Similarity 31.1%;
Matches 32; Conservative
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 6.35 Seconds 701.611 Million cell updates/sec Wed Aug 20 11:13:40 1997; Run on:

Tabular output not generated.

MASGQGPGPPRQECGEPALP.....LVVLGVVLLGQFVVRRFFKS 210 >US-08-320-157-22 (1-210) from US08320157.pep 1554 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

59021 segs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 46.936; Variance 89.738; scale 0.523

Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1.75e-27 9.85e-27 7.05e-26 6.08e-24 6.08e-24 6.08e-24 5.08e-12 1.18e-22 1.10e-11 1.00e-11 1.00e-04 1.00e-03 1.0 Pred. No. APOPTOSIS REGULATOR B
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APOPTOSIS REGULATOR B
APOPTOSIS REGULATOR B CYTOCHROME C OXIDASE HEAT SHOCK PROTEIN HT Description BC2B_MOUSE BC2A_MOUSE BCL2_RAT BAXA_MOUSE BAXA_HUMAN MCL1_HUMAN MCL1_HUMAN HSA1_MOUSE EAR_ASFE4 EAR_ASFE4 EAR_ASFE4 EAR_ASFE4 EAR_ASFE7 GOX3_CAEEL HTPG_BACSU BCLZ_CHICK BCLZ_CHICK BC2B_HUMAN BC2A_HUMAN DB Query Match Length Score Result

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THREONINE SYNTHASE (E MYOSIN LIGHT CHAIN 1, HYPOTHETICAL 37.6 KD	HYPOTHETICAL 59.6 KD HYPOTHETICAL 60.5 KD DIMETHYLANILINE MONOO HYPOTHETICAL 95.4 KD	ARG11 PROTEIN PRECURS METABOTROPIC GLUTAMAT HYPOTHETICAL 121.1 KD INOSITOL 1,4,5-TRISPH TNOSITOT. 1 4,5-TRISPH	AND THE STATE OF T	3-PHOSPHOSHIKIMATE 1- HYPOTHETICAL 54.5 KD MINOR CAPSID PROTEIN TISILD PROTEIN (EGF-R ENDOGLUCANASE E PRECU METABOTROPIC GLUTAMAT
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ALIGNMENTS

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RESULT 2 ID BCLX_RAT

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A MEDLINE; 93364977.
A BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C.E., DING L.,
BOISE L.H., GONZALEZ-GARCIA M., POSTEMA C.E., DING L.,
L. LINDSTEN T., TURKA L.A., MAO X., NUNEZ G., THOMPSON C.B.;
CELL 74:597-608(1993).
C -1- FUNCTION: DOWINANT REGULATOR OF APOPTOTIC CELL DEATH.
C -1- FUNCTION: DOWINANT REGULATOR OF APOPTOTIC CELL DEATH.
C -1- TISSUES PECIFICITY: BCL.X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
C THAT UNDERGO A HIGH RATE OF TUNOVER, SUCH AS DEVELOPING
LLONG-LIVED POSTMITOTIC CELLS, SUCH AS DEVELOPING
C LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
C -1- SIMILARITY: BELONGS TO THE BCL.2 FAMILY.
R EMBL; 223115; G510901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaswmatylndh-1 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 dspavngatghs-ssldarevipmaavkgalreagdefelryrrafsdltsglhitpgta 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-DEATH...

MICHAELIDIS T.M.;

SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH...

-!- ALTERNATIVE PRODUCTS: TWO ISOFORMS, BCX-X(L) (SHOWN HERE) AND BCL-X(S), ARE DERIVED BY ALTERNATIVE SPLICING...

-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

EMBL; X82537; G607177; -.

EMBL; X82537; G607178; -.

APOPTOSIS; ALTERNATIVE SPLICING.

APOPTOSIS; ALTERNATIVE SPLICING.

VARSPLIC 126 ... RISSING (IN BCL-X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                      RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 254; DB 1; Length 233;
Pred. No. 9.85e-27;
41; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN BCL-X(S)).
G -> A (IN G510901).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCLX_HUMAN STANDARD; PRT; 233 AA. 207817; 213 AA. 207817; 215 CREL. 31, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                          01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01080; BCL2.
APOFFOSIS; ALTERNATYE SPLICING.
126 188 MIS
CONFLICT 70 70 G - G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 epwigenggwdtfvdlygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 ARWIAQRGGWVAALNL-GNGP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.5%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APOPTOSIS REGULATOR BCL-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE STATE OF THE S
SOUTH THE SOUTH 
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                       61 dspavngatghs-ssldarevipmaavkgalreagdefelryrrafsdltsglhitpgta 119
                                                                                                                                                                            yqsfeqvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndh-1 178
                                                                                                                                                                                            60 hhrpeppgsaaasevppae-glrpapp-g-vhlalrqagdefsrryqrdfaqmsgqlhlt 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 pftahgrfvavveelfrdgvnwgrivaffefggvmcvesvnremsplvdniatwmteyl. 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 245; DB 1; Length 233;
Pred. No. 4.70e-25;
40; Mismatches 57; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
E -> S (IN REF. 2).
GSAAASEVPPAEGIRP -> ARLLIVYCPRIRGCA
                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; D11381: G222794; -i-
EMBL; D11381: G222794; -i-
EMBL; D11381: G22770; -i-
PRL; A37332; A37332.
PIR; S24390; S24390.
PIR; S24390; S24390.
APOPTOSIS; TRANSHEMBRANE; MITOCHONDRION.
TRANSHEM 208 228 POTENTIAL.
                                      Length 233;
                                                                      Indels
                                16.1%; Score 250; DB 1; Le
larity 25.5%; Pred. No. 5.51e-26;
Conservative 41; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN REF. 2).
H -> T (IN REF. 2).
G -> V (IN REF. 2).
4; 3376502C CRC32;
26049 MW; 57C67491 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                  Ö1-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                     233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLLINE, 92375724.
EGUGHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                               || : ||| : ::| || :
167 ARWIAQRGGWVAALNL-GNGP 186
                                                                                                                                                                                                                                             179 epwiqenggwdtfvelygnna 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 H
139 G
25687 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 28.5%;
41; Conservative
                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
139
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
 233 AA;
                                                Best Local Similarity
Matches 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92379084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALLIFORMES
                                                                                                                                                                                                                                                                                                                                 RESULT 4
ID BCL2_CHICK
AC Q00709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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LT 6
BC2A_HUMAN
P10415;
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
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NATURE 348:334-336(1990).

-!- FUNCTION: PROLOMOS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDARY PARHWAY TO PREVENT APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDARY PATHWAY TO PREVENT APOPTOSIS AT SITES
OF FREE RADICAL GENERATION SUCH AS MITCCHONDRIA.

-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
104 AENAYEYFTKIATSLFESG-NWGRVVALLGFGYRLALHVYQHGLTGFLGGVTRFYVDFML 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssglhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 tvveelfrdgvnwgrivaffefggvmcvesvnremsplvdnialwmteylnrh-lhtwiq 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T(14;18)(032;021) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2:
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PROTO-IN CAUGENE, APOPTOSIS, ALTERNATIVE SPLICING; MEMBRANE;
MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
SEQUENCE 205 AA; 22311 MM; ED321E5E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 15.4%; Score 239; DB 1; Length 205; Best Local Similarity 29.7%; Pred. No. 6.08e-24; Matches 38; Conservative 34; Mismatches 51; Indels
                                                                                                                                                                                                                                                                         TSUJIMOTO Y., CROCE C.M.;
PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
                                                                                                                                   01-MAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIFFER AT THEIR C-TERMINAL ENDS.
-- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL; M13995; G179369; ALT_SEQ.
PIR; B29409; TWUUB1.
PIR; D37332; D37332.
                                                                                                              205 AA
                                                                                                                                                                                                                                                                                                                                         EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
                                   177 rh-lhnwiqdnggwdafvelygns 199
                                                             163 HHCIARWIAQRGGWVAALNL-GNG 185
                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                  REVISIONS TO 96 AND 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS01080; BCL2
                                                                                                                                                                                                                                                                                                                                                                     [3]
SUBCELLULAR LOCATION.
                                                                                                                                                                          PROTEIN BCL-2-BETA.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 86259760.
                                                                                                                                                                                                                                                                                                                                MEDLINE; 92375724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 dnggwyga 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 QRGGWVAA 179
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 91066924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 151430;
                                                                                                   LT 5
BC2B_HUMAN
P10416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGIONS
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HOCKENBERY D., NUNEZ G., MILLIMAN C., SCHREIBER R.D., KORSMEYER S.J.;
NATURE 348:334-336(1990).

-!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT
FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES
OF FREE RADICAL GENERATION SUCH AS MITOCHOURIA.
-!- SUBCELLULAR LOCATION: MITOCHOURIAL INNER MEMBRANE.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE
II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION
T(14.18)(032;021) WHICH INVOLVES BCLZ AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 tpaapgaaagpalspvppvvhlt--lrqagddfsrryrrdfaemssqlhltpftargrfa 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 APADPEMVTLP-LQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMLQHLQPTAENAYEYFT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTO-ONCOGENE; APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE; MITOCHONDRION; CHROMOSOMAL TRANSLOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 239; DB 1; Length 239; Pred. No. 6.08e-24; 36; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
P -> T (IN REF. 3).
S -> R (IN REF. 3).
W; 75084B59 CRC32;
                                                                                                                                                                                                                                                                                                                                              PROC. NATL. ACAD. SCI. U.S.A. 83:5214-5218(1986).
                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIFFER AT THEIR C-TERMINAL ENDS.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL, M1994; G179367; ALT_SEQ.
EMBL, M14745; G179371; -.
PIR; A29409; TYHUAI.
PIR; A24428; TYHUBC.
PIR; C37332; C37332.
  239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
NUCLEIC ACIDS RES. 20:4187-4192(1992).
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 87002488.
CLEARY M.L., SMITH S.D., SKLAR J.;
CELL 47:19-28(1986).
                                              CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26266 MW;
                                                                                                                                                                                                                                                                                                                                                                        [2]
REVISIONS TO 96; 110 AND 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 29.3%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                TSUJIMOTO Y., CROCE C.M.;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01080; BCL2
                                           01-MAR-1989 (REL. 10,
01-APR-1993 (REL. 25,
01-NOV-1995 (REL. 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION.
                                                                                                                      PROTEIN BCL-2-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212
59
117
239 AA;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 86259760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91066924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 151430;
PROSITE; PS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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LT 9
BCL2_RAT
P49950;
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Matches
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                                                                                                                                      94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
                                                                                                                                                                                                                                                                                                                      78 LAIIGDDINRRYDSEFOTMLQHLQPTAENAYEYFTKIATSLFESG-NWGRVVALLGFGYR 136
                                                                                                                                                                                                                                                                                             Gaps
                                                                                              MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEGRINI M., SILINI E., KOZAK C., TSUJIMOTO Y., CROCE C.M., CELL 49:455-463(1987).
                                                                                                                                                                                                                                                                              Length 199;
                                                                                                                                                                                                                                                                             Score 234; DB 1; Length 199
Pred. No. 5.08e-23;
28; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                    154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwvga 195
                                                                                                                                                                                                                                                                                                                                              137 LALHVYQHGLTGFLGQVTRFVVDFMLHHCIARWIAORGGWVAA 179
                                                         01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-007-1996 (REL. 34, LAST ANNOTATION UPDATE)
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (REL. 10, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTEIN BCL-2 ALPHA.
                                              199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 221-222.
MEDLINE; 92375724.
EGUCHI Y., EWERT D.L., TSUJIMOTO Y.;
                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
     191 dnggwdafvel-ygpsmrpl 209
            172 QRGGWVAALNIGNGPILNVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-LIVER;
MEDLINE; 87187643.
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.1%;
Matches 32; Conservative
                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                             EUTHERIA; RODENTIA.
                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 87187643.
                                                                                                                                                                                                                                                                                                                                                                                                                         BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                               BC2A_MOUSE
P10417;
                                              BC2B_MOUSE
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94 lrragddfsrryrrdfaemssqlhltpftargrfatvveelfrdgvnwgrivaffefggv 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 rdtaartsplrp-lvanagpalspvppvvhltlrragddfsrryrrdfaemssglhltnf 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BLOCKS APOPTOSIS. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVEWEY APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.

-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94193015.
SATO I., IRIE S., KRAJEWSKI S., REED J.C.;
GENE 140:291-292(1994).
-!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
-!- ALTERNATIVE PRODUCIS: TWO FORMS OF BCL-2: ALPHA, AND BETA, AF
PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 mcvesvnremsplvdnialwmteylnrh-lhtwiqdnggwdafvel-ygpsmrpl 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; MIDDUD, C.C.
PIR; A25560; TVMSA1.
PIR; A25560; TVMSA1.
PROSITE; PS01080; BCL2.
APOPTOSIS; ALTERNATIVE SPLICING; TRANSMEMBRANE; MITOCHONDRION.
209 POTENTIAL.
209 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN BCL-2 ALPHA.
BCL2 OR BCL-2.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 14.9%; Score 232; DB 1; Length 236; Local Similarity 27.2%; Pred. No. 1.18e-22; nes 40; Conservative 42; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 234; DB 1; Length 236
Pred. No. 5.08e-23;
30; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 AA; 26550 MW; 336E6B40 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REL. 34, CREATED)
(REL. 34, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIFFER AT THEIR C-TERMINAL ENDS.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY EMBL; L14680; G408947; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 30.4%;
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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01-0CT-1996 (
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MEDLINE; 93364978
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Matches
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nmelgrmiadvdtdspre-vff-rvaadmfadgnfnwgrvvalfyfasklvlkalctkvp 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: :: || |: :: || :: :: || 148 GFLGQVTRFVVDFMLHCIARWIAQRGGWVAALNIGNGPI-LNVLVVLGVVLLGGFVVRR 206
                                                                                                                          targrfatvveelfrdgvnwgrivaffefggvmcvgsvnremsplvdnialwmteylnrh 181
                                                                                                                                                                                                 106 NAYEYFTKIATSLFESG-NWGRVVALLGFGYRLALHVYQHGLTGFLGQVTRFVVDFMLHH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL 74:609-619(1993).
-!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BL-2.
-!- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|:::: | : |: | | ||:: | | ||:: | |||:: ||::: | |||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCILITIE FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
-1- SUBCELLULAR LOCATION: MEMBRANE.
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
-1- STA172; G388192; -
-1- PROSITE; PS01080; BCL2.
-1- PROSITE; PS01080; BCL2.
-1- APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 206; DB 1; Length 192;
Pred. No. 5.98e-18;
49; Mismatches 75; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-07-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 AA; 21394 MW; BD035304 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                         182 -lhtwigdnggwdafvel-ygpsmrpl 206
: || : || | : | || : |
165 CIARWIAQRGGWVAALNLGNGPILNVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Best Local Similarity 25.6%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL/6 X DBA/2 F1;
MEDLINE; 93364978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAXA_MOUSE
Q07813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAXA_HUMAN
Q07812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT OF THE SULT OF THE SULT
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BAC 000
AC 000
DT 001
DT 010
DT 010
DC 000
CC CC CC
RN C CC
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HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.

SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 gdragrmggeapelaldpvpgdastkklseclkrigdelds--nmelgrmlaavdtdspr 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                          -!- SUBCILITIE FORMS HOMOIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
-!- SUBCELLUIAR LOCATION: MEMBRANE.
-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS. BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
-- EMBL. 1.22473; G388166; -.
-- PIR; A47538; A47538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELDINGS TO THE BCL-2 FAMILY.
EMBL; L22474; G388168; -.
PIR; B47538; B47538.
OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
CELL 74:609-619(19193).
-1- FUNCTION: ACCELERAFES PROGRAMMED CELL DEATH BY BINDING TO THE
APOPTOSIS REPRESSOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO THE APOPTOSIS REPRESSOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                        Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 218
                                                                                                                                                                                                                                                                                                                                                                        / Match 12.5%; Score 194; DB 1; Length 192
Local Similarity 24.5%; Pred. No. 7.87e-16;
nes 40; Conservative 44; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 189; DB 1; Length 218
Pred. No. 5.86e-15;
35; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 rllgwiqdqggwdgllsyfgtptwqtvtifvagvltasltiwk 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q07814;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
APOPTOSIS REGULATOR BAX, CYTOPLASMIC ISOFORM BETA.
                                                                                                                                                                                                                                                                                         APOPTOSIS; TRANSMEMBRANE; ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82B2FF09 CRC32;
                                                                                                                                                                                                                                                                                                              172 192 POTENTIAL.
192 AA; 21184 MW; B2E6148A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93364978.
OLTVAI Z.N., MILLIMAN C.L., KORSMEYER S.J.;
CELL 74:609-619(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRÓSITE; PS01080; BCL2.
APOPTOSIS; ALTERNATIVE SPLICING.
SEQUENCE 218 AA; 24220 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.2%;
Best Local Similarity 27.0%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                    PROSITE; PS01080; BCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-B-CELL
                                                                                                                                                                                                                                                 600040;
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EUTHERIA; PRIMATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 lyrqsleiisrylreqatgakdtkpmgrsgatsrkaletlrrygdgyqrnhetvfqgmlr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 kldikneddvkslsrvmihvfsdgvtnwgrivtlisfgafvakhlktingescieplaes 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 FYRHQQEQEAEGVAAPADPEMVTLPLQPSSTMGQVGRQ-LAIIGDDINRRYDSEFQTMLQ 98
gdragrmggeapelaldpvpgdastkklseclkrigdelds--nmelgrmiaavdtdspr 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 93.34-28.

MEDLINE; 93.34-28.

PROC. NATL. ACAD. 1. BUCHAN H.L., ZHOU P., CRAIG R.W.;

PROC. NATL. ACAD. SCI. U.S.A. 90:3516-3520(1993).

-I- FUNCTION: INVOLVED IN PROGRAMMING OF DIFFERENTIATION AND CONCOMITANT MAINTENANCE OF VIABILITY BUT NOT OF PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       baa.
Homo Sapiens (Human).
Eukarkota; metazoa; Chordata; Vertebrata; Tetrapoda; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                       MCLI_HUMAN STANDARD; PRT; 350 AA.
007830;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 176; DB 6; Length 350;
Pred. No. 1.00e-12;
39; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR A. POTENTIAL. ; 10194B64 CRC32;
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01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BAX PROTEIN, CYTOPLASMIC ISOFORM DELTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-MYELOID LEUKEMIA CELLS;
MEDLINE; 93234528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 itd-vlvrtkrdwlvkgrgw 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.3%;
Matches 34; Conservative
                                                                                                                                                                                                                                           147 rllgwigdgggwyrllk 163
                                                                                                                                                                                                                                                                                                    165 CIARWIAQRGGWVAALN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 14
BAXD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: INTRACELLULAR.
-:- TISSUE SPECIFICITY: EXPRESSED IN HEMOPOLETIC TISSUES, INCLUDING
BONE MARROW SPLEEN AND THYMUS.
-:- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL. 116462; G293274; -..
APOPTOSIE; PS01080; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                         APTE S.S., MATTEI M.-G., OLSEN B.R.;
GENOMICS 26.592-594(1995).
-I - ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASHIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
-I - SUBCELLULAR LOCATION: CYTOPLASHIC (POTENTIAL).
-I - SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
EMBL, U19599; G841238; -
-MIM; 600040; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIN E.Y., ORLOPSKY A., BERGER M.S., PRYSTOWSKY M.B.;
J. IMMUNOL. 151:1979-1988(1993).
-!- FUNCTION: MAY FUNCTION IN THE RESPONSE OF HEMOPOIETIC CELLS TO
EXTERNAL SIGNALS.
-!- INDUCTION: BY GRANULCCYTE-MACROPHAGE COLONY-STIMULATING FACTOR
AND LPS IN MACROPHAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 rivtifafggvllkklpqeqialdvcaykqvssfvaefimnn-tgewirqnggw 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                       Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 172;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HEMOPOIETIC-SPECIFIC EARLY RESPONSE PROTEIN (A1 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 lrerllgwigdaggwdgllsyfgtptwqtvtifvagvltasltiwk 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                10.6%; Score 165; DB 1; 727.4%; Pred. No. 7.08e-11; ative 30; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 10.2%; Score 158; DB 5; I
Local Similarity 28.1%; Pred. No. 1.01e-09;
Nes 32; Conservative 29; Mismatches 46;
                                                                                                                                                                                                                                                              APOPTOSIS; ALTERNATIVE SPLICING.
SEQUENCE 143 AA; 15772 MW; 71AA1CBD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN 24 33 ALA/PRO-RICH.
SEQUENCE 172 AA; 19914 MW; FFD38D6F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
STRAIN=CBA,J; TISSUE=BONE MARROW;
MEDLINE; 93346743.
                                                                                                                                                                                                                                                                                                                                                        larity 27.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                 t Local Similarity
ches 29; Conser
SEQUENCE FROM N.A. MEDLINE; 95331797.
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HSA1_MOUSE
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Search completed: Wed Aug 20 11:14:06 1997 Job time : 26 secs.

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